Perfect score: Scoring table:

Run on:

Sequence:

gb_ba:* gb_htg:* gb_in:* *: WO_

Database :

Query Score Match Length DB No. Result

em_in:*
em_om:*
em_or:*
em_ov:*

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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

I (bases I to 145123)

S Akhter, N. Ayele, K. Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S. C., Mackeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Frasad, A., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Malker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.H. and Green, E.D.
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5 ordered
                                                                                                  Cambridge, Downing
Tsolation and characterization of microsatellites in albatrosses Mol. Ecol. 8 (2), 338-341 (1999) 99164945.
2 (bases 1 to 661)
Burg, T.M.
Burg, T.M.
Submitted (05-0CT-1998) Zoology, University of Cambridge, Downing Street, Cambridge CB2 3EJ, UK
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                                                                                                                                                                                                                                                                                                                                                                                                   267 AAGTATTTAAAAGATGTGGCACTTAGGGACATGGTTTAGTGGACATGGTGGTGTTGGGTT 208
                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-JUL-2001) NIH Intramural Sequencing Center, 8 Grovemont Circle, Gaithersburg, MD 20877, USA On Jan 30, 2002 this sequence version replaced gi:14595776.
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Center code: NISC
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0; Mismatches 35;
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Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
                                                                                                                                                               /organism="Diomedea exulans"
/db_xref="taxon:46550"
1. .661
/note="microsatellite De2"
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AC092403.2 GI:18425282
HTG; HTGS_PHASE2; HTGS_DRAFT.
chicken.
                                                                                                                                                1. .661
/organism="Diomedea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 TAATTTTATTCTTGATCTTTTGAGC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 TGATTCTATGAAAGATGTATGTATGC 123
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185 c 127
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                                                                                                                                                                                                                                                                                                       Query Match 10.8%;
Best Local Similarity 75.3%;
Matches 110; Conservative
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                                                                                   TITLE
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Archosauria; Aves; Neognathae; Procellariiformes; Diomedeidae;
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                                                                 Mismatches
                                    100.0%; Score 723; 100.0%; Pred. No. 4
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Diomedea exulans microsatellite
AF096788
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Burg, T.M.
                                                                   723; Conservative
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Diomedea exulans
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated established using one of each sequence contig has been deat from individual subclones, overlaps with neighboring human), and/or confirmation by PCR testing. In addition, coverage in QOD Bases and has been reviewed to rule out gross missasemblies, the low-quality ends of sequence on the sequence assembly is based on at lasst 8% average grooss missasemblies, the low-quality ends of sequence ontigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

Sequencing vector: plasmid; n/3: 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap: version 0.990319 consensus quality: 14343 bases at least QAO Consensus quality: 14412 bases at least QAO Consensus quality: 14412 bases at least QAO Insert size: 143700: agancose-fp Insert size: 14373; sum-of-contigs Quality coverage: 12.65x in Q20 bases; sum-of-contigs
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**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

**The finished sequence as soon as it is available and the accession number will be preserved.

**The finished sequence as soon as it is available and the accession number will be preserved.

**The finished sequence as soon as it is available and state of $191 contig of $391 bp in length $192 contig of $1938 bp in length $195 contig of $1938 bp in length $195 contig of $1938 bp in length $192 contig of $1938 bp in length $192 contig of $1938 bp in length $192 contig of $2314 bp in length $192 con
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1. .5391
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760te-"assembly_fragment"
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760te-"assembly_fragment"
76002081 clone overlaps with GenBank Accession Number AC092081 clone 77019 (center project name apl)"
760te-"assembly_fragment"
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="100N11"
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Center project name: apk
Center clone name: 100N11
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8.7%; Score 62.8; DB 2; Length 145123;

Query Match

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ISM Gallus gallus

Gallus gallus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianine; Gallus.

Callus.

(Dases 1 to 1124309)

RS Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,

Granite,S., Guan, X., Gupta,J., Ho,S.-L., Indol,J.R., Karlins,E.,

Lee-Lin,S.-Q., Legaspi,R., Lim,M., Maduro,Q.L., Maduro,V.B.,

Phomas, J. W., Thomas,P. J., Touchman,J.W., Tsurgeon,C., Vogt,J.L.,

Malker,M.A., Wetherby,K.D., Zhang,L.H. and Green,E.D.

MISC Comparative Sequencing Initiative

RS Chases 1 to 124309)
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Db 71754 TGGACAGCTGGGCTAGATGATCTCAGAGGTCTTTTCCAACCTTAATGATCTATGATT 71697
                                           1; Gaps
                                                                       16 CAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGACAAGGTGA-TGGTTGG 74
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Submitted (24-MAY-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 124309)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-001) NIH Intramural Sequencing Center, 8717 Growenort Circle, Gatthersburg, MD 20877, USA On Aug 9, 2001 His sequence version replaced gi:14192887.
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Best Local Similarity 76.3%; Pred. No. 0.00044;
Matches 90; Conservative 0; Mismatches 27; Indels
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Web Site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
Center project informetion
Center project name: apo
Center clone name: 068C05
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/db_xref="taxon:9031"
/clone="68C5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zosterops lateralis chlorocephala.
Sosterops lateralis chlorocephala.
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Zosteropidae;
                                                                                                                                                                                                                                                                              Db 71279 TTCAAGAAACATGGAGAGGTGGCACTGAGGGACATGGTTACAGGGCATGGTGGTGATGG 71338
                                                                                                                                                                                                                                                                                                                                     Db 71339 GCTGATGGTTTGACTAGATGGTCTTAGAGGTCTTTTCCAACCTCAGTGATCCTATGAA 71396
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                                                                                                                                                                                                                                                                                                                       74 GTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTTCCAGCCTTAATAATTCTATGAA 131
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                                                                                                                                                                                                     8.6%; Score 62; DB 5; Length 124309; 70.3%; Pred. No. 0.00067;
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/sub_species="chlorocephala"
/db_xref="taxon:79321"
/clone="ZL22"
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Pred. No. 0.0025;
0; Mismatches 33; Indels
gallus-Red Jungle Fowl
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/rpt_unit=gt
complement(142. .165)
51 c 42 g
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 /clone_lib="GGR-G.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianiae; Gallus.

1 (bases 1 to 156014)

Rattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totokl,Y., Watanabe,H. and Sakaki,Y. Homo saplens genomic DNA

Published Only in Database (2001) In press

E (bases 1 to 156014)

Rattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totokl,Y., Watanabe,H. and Sakaki,Y.

Rujiyama,A., Yada,T., Totokl,Y., Watanabe,H. and Sakaki,Y.

Eujiyama,A., Yada,T., Totokl,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

NL Shii,K., Totokl,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Submitted (27-2UN-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori)gesc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

On Oct 19, 2001 this sequence version replaced gi:15208285.

This work was done in collaboration with Yokomine, T. and Sasaki,
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   92 TGATCTCAGAGTTTTTTCCAGCCTTAATAATTCTATGAATTCTGTAATTTTAT 145
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64.6%; Pred. No. 0.0024;
iive 0; Mismatches 56;
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1-111, Yata, Mishima, Shizuoka, JAPAN
zip: 411-8540
e-mail: hisasaki@lab.nig.ac.jp.
Location/Qualifiers
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/db_xref="taxon:9031"
/chromosome="5"
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nrvv3/95 187259 bp DNA linear VRT 20-OCT-2001 Gallus gallus genomic DNA, chromosome 5, clone:192C9, complete sequence.
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                                                                                                                                                                                                                                                                               9774 ATTAGTGGTAGGTGGATAGTTAGACTAAATGCTGTTGGGGGTCTTTTCCAGCCTTAATGA 9833
                                                                                                                                                                                                 64 GTGA-TGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAATAA 122
                                                                                                                                 1; Gaps
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                                                                                     Query Match

8.0%; Score 57.8; DB 5; Length 31793;
Best Local Similarity 68.6%; Pred. No. 0.0066;
Matches 94; Conservative 0; Mismatches 42; Indels 1;
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1-111, Yata, Mishima, Shizuoka, JAPAN
2ip: 411-8540
e-mail: hisasaki@lab.nig.ac.jp.
Location/Qualifiers
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/db_xref="taxon:9031"
/chromosome="5"
/map="5"
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/product="T-cell receptor alpha chain"
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//note=""-cell receptor alpha chain"
/complement(join(17609. 17806,18313. 18461,20122. 20371))
                   GGUB3833 31793 bp DNA linear VRT 01-0CT-1997 Gallus gallus T-cell receptor alpha chain gene, partial cds, and defender against death protein 1 (DADI) gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSGTAGSGVGAAGSVGSVVRRFLAEYGSGTSSRLKVLDAYLLYV
MLTGALQFGYCLGGTGFPRNSFLSGFTSAVGSFILGVCLRIQINPQNKGEFGGISPER
AFADFLFANTILHLVVINPYG"
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join(<8391. .8654,9095. .9142,10211. .10317,10786. .10791)
                                                                                                                                                                 Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
1 (bases 1 to 31793)
                                                                                                                                                                                                                                                           Wang, K., Gan, L., Kuo, C. L. and Hood, L. A highly conserved apoptotic suppressor gene is located near the chicken T-cell receptor alpha chain constant region Immunogenetics 46 (5), 376-382 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-JAN-1997) Genomics, Darwin Molecular Corp., 1631
220th St. SE, Bothell, WA 98021, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /drogansm="Gallus gallus"
/db_xref="taxon:9031"
<567. .>629
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<5504, >>5524, >>5524

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/note="putative T-cell receptor joining region"
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/qene="DAD1"
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/protein_id="AAC60278.1"
/db_xref="G1:2149252"
                                                                                                                                                                                                                                                                                                                                                                                             Wang, K., Gan, L., Kuo, C.L. and Hood, L.
Direct Submission
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/codon_start=1
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Robasianiane; Gallus.

E 1 (bases 1 to 10956)

S Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X. Gupta, J., Maduro, Q.L., Maduro, W.B., Masiello, C., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, W.B., Masiello, C., Shevchenko, Y., Snyder, B., Stantripop, S., Thomas, J.W., Phomas, P.J., Tiongson, E. Touchman, J. W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                               VRT 26-JAN-2001
                                        1. .109569

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64635 GGAGGTGCTCAGGAACATGGAGATATAGCACTGAGGGACGTGGTCAGTGAGCAATATTGG 64576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (15-NOV-2000) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 109569)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest.
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                                                                                                                                                                                                                                                                               linear
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Gallus gallus clone 65N20, complete sequence.
ACO84760
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------- Project Information
Center project name: apc
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To (bases 1 to 156014)
Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
Homo sapiens genomic DNA
Published Only in Database (2001) In press
2 (bases 1 to 156014)
Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Bulnet Submission
Submitted (27-JUN-2001) Masahira Hattori, The Institute of Physical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This work was done in collaboration with Yokomine, T. and Sasaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                     Score 55.4; DB 5;
Pred. No. 0.018;
0; Mismatches 46;
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/note="single clone coverage"
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/organism="Gallus gall
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Chicken.

Archosauria; Aves; Neognathae; Craniata: Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Dassa 1 to 124309.

Mayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,

Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L.,

Granite, S., Guan, X., Gupta, J., Ho, S.-L., Idol, J.R., Karlins, E.,

Mastello, C., Mastrian, S.D., McCloskey, J.G., McDowell, J.,

Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stantripop, S.,

Thomas, J.W., Thomas, P.J., Touchman, J. W., Tsurgeon, C., Vogt, J.L.,

Walker, M.A., Wetherby, K. D., Zhang, L. H. and Green, E.D.

WISC Comparative Sequencing Initiative
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Diagnosis of diseases associated with the immune system
Patent: W0 020038-A 690 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
1. 12007
/organism="synthetic construct"
/db_xref="taxon:325630"
/oce="chemically treated genomic DNA (Homo sapiens)"
3266 a 114 c 2487 g 6140 t
                                                                                                                                                                                                                                                                                                                                                                   103 TTTTTTTCCAGCCTTAATAATTCTATGAATTCTGTAATTTTATTCTTGATCTTTTTGAGC 162
                                                                                                                                                                                                                                                                                                                                                                                                                     223 ACTITCATITGCAACAFGAGAATIGCTGTATITGTCAGGTTACAAGTAGTGCAATGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 CTTAGAAGTAGTGAGAAACATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 CCAAACTGTAGCTTTGGGATTTGAGGAGCCACAGAGTTGTATAAATTTGTTTAATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.6%; Score 54.8; DB 6; Length 12007;
46.6%; Pred. No. 0.034;
tive 0; Mismatches 202; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC091708 124309 bp DNA 1
Gallus gallus clone 68C5, complete sequence.
AC091708 2 GI:15145070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 TTTTTTTGGCTTCTTCA 480
                                                                                                                                                                                                                                                                                  Best Local Similarity 46.69
Matches 176; Conservative
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Direct Submission
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Best Local S
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianiae, Gallus.
1 (bases 1 to 5805)
Staines, D.M. and Thomas, J.O.
A sequence with homology to human HPFH-linked enhancer elements and
to a family of G. profein linked membrane receptor genes is located
downstream of the chicken beta-globin locus
Gene 234 (2), 345-352 (1999)
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Submitted (03-NOV-1998) Thomas J.O., Department of Biochemistry,
University of Cambridge, 80 Tennis Court Road, Cambridge, CB2 1GA,
University of Cambridge, 80 Tennis Court Road, Cambridge, CB2 1GA,
                                                         10295 GGTCAACGGTTGGACTTTAGAGGTCTCTTCCAACCTTAATGATATGATGACT 10226
                                                                                                               73 GGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAATAATTCTATGAAT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 TTCAAGGAAAGGGTGGATGTAGTAATTAGGACACAGTTCATTGGGAAATACTGGGGTAG 358
    Gaps
                                     14 ITCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGACAA-GGTGATGGTT 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 GTCAAAAGTIGGACTCGATGATCTCAGAGTTTTTTCCAGCCTTAATAATTCTATGAAT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence starts
11.5 kb downstream of the 3'-end of the epsilon-globin gene Related sequences 279587, X91835, A60547.
Location/Qualifiers
                                                                                                                                                                                                                  Gallus gallus DNA sequence downstream of beta-globin locus. AJ012570 GI:4995211
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    1;
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    Indels
  33;
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/note="ORF; possible pseudogene"
1355 c 1495 g 1437 t
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  0; Mismatches
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/organism="Gallus gallus"
/db_xref="taxon:9031"
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synthetic construct
artificial sequence.
  Conservative
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                                                                                                                                                                                                                                                                                                                                             chicken.
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86;
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GGA012570
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AX345619
  Matches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

E 1 (bases 1 to 165108)
S Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Boulfard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho.S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, O.L., Maduro, V.E., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

NISC Comparative Sequencing Initiative
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                                                                                                                                                                                                    Genomic DNA sequence from a DNA library from turkey microsatellites
                                                                                                                                                                                                                                                                                                                                              Submitted (08-DEC-1998) Comparative Genomics, Tuskegee University, 109 Milbank Hall, Tuskegee, AL 36088, USA Location/Qualifiers
                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Meleagrididae,
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Submitted (20-JUN-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Jan 30, 2002 this sequence version replaced gi:14495366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 TTCAAGGAATGACTAGATGTGCCACTTAGTGCCCATGGTCTAGTTGACAAGGTGATGGTTG 73
                                                                                                                                                                                                                                                                          Smith, E.J., Nahason, S., Shi, L., Drummond, P., Zahorchak, R. and
                                                                                                  1. (bases 1 to 314)
Smith,E.J., Nahason,S., Shi,L., Drummond,P., Zahorchak,R.
Foster,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.5%; Score 54.2; DB 5; Length 314; Best Local Similarity 71.4%; Pred. No. 0.077; Matches 85; Conservative 0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
0.077;
33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Meleagris gallopavo"
/db_xref="taxon:9103"
/clone="TUCA930"
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/note="microsatellite"
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AC092081.2 GI:18425283
HTG: HTGS_PHASE2; HTGS_DRAFT.
Chicken.
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84 c 56
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                            Meleagris gallopavo
                                                                                                                                                                                                                                                     (bases 1 to 314)
                                                                                                                                                                                                                                                                                                    Foster, J.C.
Direct Submission
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AC092081/c
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UCD001-pBeloBAC11/BI BAC library"
11962. .12098
/note="single clone coverage"
83376. .>124309
/note="this sequence is not the entire insert of clone
6865; clone overlaps with GenBank Accession Number
AC084760 (nucleotides 1-52406) clone 65N20 (center project
nucleotides 1-40929 of AC084760"
a 25022 c 24937 g 36906 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 11478 TGATGGCTGATGATTGAACTGGGTGATCTTAGTGGTCTTTTCCAACCTAACTGATTCGA 11419
                                                                Green, E.D.
Direct Submission
Submitted (09-AUG-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
Grovemont Circle, Gaithersburg, MD 20877, USA
On Aug 9, 2010 this sequence version replaced gi:14192887.
Submitted (24-MAY-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 124309)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality and constity >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil3 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 GGAGGTTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGACAAGGTGA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlapp are noted in the beginning and end of the Peatures section.
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Meleagris gallopavo clone TUCA930 microsatellite sequence.
AF111666.1 GI:5911090
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                                                                                                                                                                                                                                              Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="68C5"
                                                                                                                                                                                                                                                                                                                                                                               Center clone name: 068C05
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FEATURES

Query Match

BASE COUNT

Local

Best Loca Matches

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RESULT 14 AF111666/C

DEFINITION ACCESSION VERSION KEYWORDS

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misc_feature

clone_end:T7

/note="clone overlaps with GenBank Accession Number AC092403 clone 100N11 (center project name apk)"

misc_feature

misc_feature misc_feature misc_feature

misc_feature

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Anote="assembly_fragment"
52187..108036
Anote="assembly_fragment"
108137..165108
Anote="assembly_fragment"
clone_end:sP6

vector_side:right"

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                                                                                                                                           14 TTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGACAAGGTGATGGTTG 73
                                                                  Query Match 7.4%; Score 53.8; DB 2; Length 165108; Best Local Similarity 65.3%; Pred. No. 0.038; Matches 79; Conservative 0; Mismatches 42; Indels 0;
  400 others
  45540 a 36404 c 37447 g 45317 t
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BASE COUNT
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Mon Aug 5 11:51:35 2002

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 2, 2002, 13:28:39; Search time 8940.62 Seconds (without alignments) 1091.457 Million cell updates/sec Run on:

US-08-973-363-1 723 1 CCCGGTCGGAGGTTTCAAGG......CTTGAAACCTCCCGACCGGG 723 Title: Perfect score:

Seguence:

13736207 seqs, 6748477542 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

27472414 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

EST: * Database :

em_estba:*
em_esthum:*
em_estin:*
em_estro:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AL585441 AL584441 AL07432 Droscophil AL07432 Droscophil AL097701 Droscophil AG077527 Pan trogil AJ233092 Gallus ga AL57529 AL588169 AL588169 AL588169 AL514935 AL514935 AL584261 AL584261 AL514935 AL514935 AL514251 AL584261 AL514273 Droscophil AJ2466046 Gallus ga AL072604 Droscophil AL07379 Droscophil AL07309 Droscophil AL073060 Droscophil AL073060 Droscophil AL073060 Droscophil AL073060 Droscophil	
SUMMARIES	AL58541 CNSOUTT AJ39878 CNSO0262 AG077527 GGA340114 AL57229 AL51435 AL51435 AL51435 AL51435 AL51435 GGA34604 CNSO05RL GGA366046 CNSO000DR CNSO000DR	
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Score	80000 0 0000000 40000000 40000000000000	
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/dab_host="sold cells (kanamycin resistant)"
/dab_host="sold cells cells (kanamycin resistant)"
/dote="vector: pBLUBSCRIPT SK; Site_1: EcoAl; Site_2: Xhol
/cloned unidirectionally. Primer: Oligo dT. Uni-2AP XR
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CNS0301Z CNS0301Z CNS0301Z AOS7656E CNS0387F BM115695 CNS0387F CNS03877 CNS00BC CNS0DBC CNSDBC	3, 020 E	, n da	Location/Qualifiers Location/Qualifiers 1. 368 /organism="Gallus gallus" /db_xref="taxon:9031" /clone="RoS023H05" /clone="RoS023H05" /clone="lib="Statagene Chi
70777	agene Ch CDNA Clo :1316417 azoa; Ch azoa; Neo	Embryo 1) Aurray nd Bioin nn, EH25 527 4200 140 0434	/Qua n="Ga n="tay ROS0; ib=";
\$89 \$83 \$803 \$803 \$103 \$103 \$100 \$100 \$100 \$100 \$100 \$1	tratilus lus lus Met. Met. 1 to 1 to 1 to	Murray, F. Stratagene Chick Emi Stratagene Chick Emi Suppliabled (2001) Contact: Frazer Murr Dept. Genomics and i Roslin Institute Roslin, Midlothian, Tel: +44 (0)131 440 Fax: +44 (0)131 440 Fax: Hazer.murray	Location, 1.368 /organism/db_xrefr/ /clone_"/
VVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVVV	AL585441 AL585441 S 6341us gal AL58544 I AL585441.1 AL585441.1 Chicken. Chicken. Chicken. Archosauri Archosauri Archosauri Archosauri Archosauri Archosauri Archosauri Archosauri Archosauri	Murray, F. Stratagene (Unpublisher) Unpublisher Contact: Fred Dept. Genomi Roslin Insti Roslin Insti Roslin, Midl Tel: +44 (0) Fax: +44 (0)	.
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1118 1119 1119 1119 1119 1119 1119 1119	RESULT 1 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AUTHORS TITLE JOURNAL COMMENT	FEATURES SOUFCE
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AJ398678 AF2426 Gallus gallus cDNA clone 7a16r1, mRNA sequence.
AJ398678
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                                                                                                                                                          223 ACTITCATITGCAACATGAGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCAATGGCTG
                                                                                                                                                                                                 283 CTTAGAAGTAGTGAGAAACATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTG
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RRCI-98 and was constructed by partial EcoRI digestion of Inosophila DNA provided by the BDGP from the isogenic strain v2: no bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNSOOITT 974 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR37D06 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                      GATGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAATAATTC 125
                                                                                                                                                                                                                                                            TTTTTTTCCAGCCTTAATAATTCTATGAATTCTGTAATTTTATTCTTGATCTTTTGAGC 162
                                                                                                                     Gaps
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/db_xref="taxon:7227"
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72.3%;
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Abdrakhmanov, I., Lodygin, D., Geroth, P., Arakawa, H., Law, A., Plachy, J., Korn, B. and Buerstedde, J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                         Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Martinistr. http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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154 c 115 g 157 t
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73.0%; Pred. No. 3.7;
iive 0; Mismatches 33;

    .630
    /organism="Gallus gallus"

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/clone_lib="dkfz426"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'EUGP) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                           GSS 26-JUL-1999
                                                                                                                                                                               Drosophila melanogaster genome survey sequence T7 end of BAC BACNOIA10 of DrosBAC library from Drosophila melanogaster (fruit AL097301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 -CCTGTCACTGTTTTCTTTCCTTGAAACTGACTTTCATTTGCAACATGAGAATTGCTGTA 252
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561 GTGGTAGGTTGGATTGGATTGGTCTTAGAGGTCTTTTCCAACCTTAATGATTCT 502
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
(bases 1 to 1101)
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llarity 28.2%; Pred. No. 5.3;
Conservative 127; Mismatches 224; Indels 5;
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/clone="BACN01A10"
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                                           127 ATGAAT 132
                                                                                  501 ATGATT 496
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Fullyma.A. Hattorl,M., Toyoda,A., Taylor,T.D., Yada,T., Torotki.Y., Watanabe,H. and Sakaki,Y. Direct Submission
Direct Submission
Submitted (02-AdG-2001) Asso Fullyma, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mall-Chimpessigsc.riken.go.jp, URL.http://hgp.gsc.riken.go.jp/, Fel.sil-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-072A24.F.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS 03-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             AGU77527 804 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-072A24.F, genomic survey sequence.
AG077527
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                         103 ITTTTTTCCAGCCTTAATAATACTTCTATGAATTCTGTAATTTTATTCTTGATCTTTTTGAGC 162
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                                                     373 ACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCCCCTGCCTTCCATTAATTGCTTG 432
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BAC end sequences of Library PTB
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/clone_lib="PTB Chimpanzee Male BAC Library"
0 c 1 g 0 t 316 others
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8.0%; Score 58; DB 12; Length 80.
Best Local Similarity 28.3%; Pred. No. 9.5; 9.5
Matches 115; Conservative 0; Mismatches 291; Indels
Matches 115.
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/db_xref="taxon:9598"
/clone="PTB-072A24.F"
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R.Site 1 : SacI
R.Site 2 : SacI.
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Differences in gene density on chicken macrochromosomes and
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Smith,J., Bruley,C.K., Paton,I.R., Law,A.S., Masabanda,J.,
Waddington,D., Fries,R. and Burt,D.W.
Direct Submission
Submitted (12-MG-1998) Division of Molecular Biology, Roslin
Institute, Roslin, Midlothian BH25 9PS, Scotland, UK
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/organism="Gallus gallus"
/db_xref="taxon:9031"
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Anim. Genet. 31 (2), 96-103 (2000)
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Best Local Similarity 67.2%;
Matches 80; Conservative
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215 c
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GGA340114
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RESULT

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cs0Dl061xPla8"
/clone_lib="LTI_NED06_PL2"
/tissue_type="placenta"
/clone_lib="LTI_NED06_PL2"
/tissue_type="placenta"
/note="vector: pcWvSpORT 6; Site_l: NotI; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSpORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies. a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email: fliang@lifetech.com URL : http://fullength.invitrogen.com"

23 a 63 c 44 g 473 t 80 others
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bp mRNA linear EST 16-FEB-2001 sapiens cDNA clone CS0DI061YP18 3
                                                                                                                                                                                                                  Euteleostomi;
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                                                                                                                                                                                                                                                              1 (bases 1 to 883)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 ATCTTTTGAGCGAAGTTTGTTTGGGGATTTTAGTTTGGTTTCCCTGTCACTGTTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 TCCTTGAAACTGACTTTCATTTGCAACATGAGAATTGCTGTATTTGTCAGGTTACAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 ACAGTGGTACTGCCAAACTGTAGCTTTGGGATTTTGAGGAGCCACAGAGTTGTATAAAT
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                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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13;
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41.0%; Pred. No. 13;
Live 28; Mismatches 215; Indels
883 HOMO
AL575329
AL575329 LTI_NFL006_PL2
                                                 prime, mRNA sequence.
AL575329
AL575329.1 GI:12936390
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Best Local Similarity 41.0%
Matches 169; Conservative
                                                                                                                                                                                         Homo sapiens
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ALSWAZEL Stratagene Chick Embryo Lambda cDNA Library (* 937405)
Gallus gallus cDNA clone ROS006G07, mRNA sequence.
ALSWAZEL GI:13162992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .63 GAAGTITGTITGGGGATTITAGTITGGTITCCCTGTCACTGTITTCTTTCCTTGAAACTG 222
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Genoscope - Centre National de Sequencage
BED 191 9106 EVRY Cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1...619
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 619)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Match
Local Similarity 43.88', Pred. No. 16.
Local Similarity 43.88', Pred. No. 16.
No. 18.
Conservative 2. Mismatches 226; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 ITTITITIGCCTICTICATATCCTGTGGTAATGAGTTAATGCATTT 508
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Gallus gallus
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Matches
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                  ALS88169 BP Chicken Brain Library Gallus gallus cDNA clone ROSG68E07, mRNA sequence.
                                                                                                                                              Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 585)
                                                                                                                                                                                                                                                                                                                                                            Email: frazer.murray@bbsrc.ac.uk
GCGGCCGCTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
(*6854-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 GTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAATAATTCTATGAATT 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 TTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGACAAGGTGATGGTTG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.9%; Score 56.8; DB 9; Length 585; 72.1%; Pred. No. 17; tive 0; Mismatches 32; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="BP Chicken Brain Library"
/tissue_type="Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="ROS068E07"
                                                                                                                                                                                                                                                        Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin institute
                                                                                                                                                                                                                                                                                                                      Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Unknown"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .585
                                                                                                                                                                                                                                           BP Chicken Brain Library
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                                                                                                  AL588169.1 GI:13193203
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Matches 88; Conservative
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                                                                                                                                 chicken.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 CT 135
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Tel: 215-898-9384
Fax: 215-898-8780
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                                                                                                                                                                                                                                                                                                                                                  AJ393303 AKfz426 Gallus gallus cDNA clone 15a5r1, mRNA sequence.
AJ393303
                                                                                                                                                                                                                                                                                                                     /clone_lib="Stratagene Chick Embryo Lambda cDNA Library (*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Law, A., Plachy
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Gallus gallus
Galwaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 T-GATGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTCCAGCCTTAATAAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 799)
Abdrakhmanov, I., Lodygin, D., Geroth, P., Arakawa, H., Law, A., Pl, J., Korn, B. and Buerstedde, J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
20568495
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 GIGGAGGCATICAAGAAATGTGTAGATGTGGTACTAAGGAGCATGGTTTAGTGGGCAGTG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 GTCGGAGGTTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGACAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.8%; Score 56.2; DB 9; Length 716; 69.8%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Indels
                                                                             Stratagene Chick Embryo Lambda cDNA Library Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                        /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                         /clone="ROS006G07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ393303.1 GI:7122030
                                                 (bases 1 to 716)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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JOURNAL
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B13042
T30M24-Sp6.1 TAMU Arabidopsis thaliana genomic clone T30M24, DNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1147)
Fengy J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and BAC End Sequences at ATGC
Unpublished (1997)
Contact: Ecker J.
Contact: Ecker J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dept. of Biology, University of Pennsylvania, Philadelphia, PA 19104
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 CAAAGATTTACATGGTATAATGGACATGGTGGTGATAGGTCAAAGGTTGGACTAGGTGAT 85
                                                                                                                                                                                                                                                                                                                                                                                                                              Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                    Length 799;
                                                                                                                                                                                                                                        7 others
                                                                                                                                                                                     /clone_lib="dkfz426"
/tissue_type="Bursa of Fabricius"
| 145 c | 135 g 274 t
                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                  25;
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/strain="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                  7.7%; Score 55.8; D 73.4%; Pred. No. 20; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 CICAGAGITITITICCAGCCTTAATAATICTAIG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jecker@atgenome.bio.upenn.edu
Seg primer: Sp6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Gallus gallus"
/strain="CB"
/db_xref="taxon:9031"
/clone="15a5r1"
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University of Pennsylvania
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High quality sequence stop: 292.
Location/Qualifiers
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/clone_lib="TAMU"
/sex="hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B13042.1 GI:2094174
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/organism="Drosophila melanogaster"

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Query Match
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GGA246046/c
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR12F23 of RPCI-98 library from Drosophila melanogaster (fruit
fly) agnomic survey sequence.
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                                                                                                  51 TCTAGTTGACAAGGTGATGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTC 110
                                                                                                                                                             111 CAGCCTTAATAATTCTAATGAATTCTGTAATTTTATTCTTGATCTTTTGAGCGAAGTTTG 170
                                                                                                                                                                                                                                                               231 TTGCAACATGAGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCCAATGGCTGCTTAGAAG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 TAGTGAGAAACATTTAGGGAAATACTGGAGTGAAGCAAAACACAGTGGTACTGCCAAACTG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 TAGCTTTGGGATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCC 410
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Prerygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 919)
                                        ö
   26.2%; Pred. No. 16;
tive 0; Mismatches 338; Indels
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Drosophila melanogaster
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Best Local Similarity 26.2 Matches 120; Conservative
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GGA246046 411 bp DNA linear GSS 21-JUN-1999 Gallus gallus anonymous sequence from cosmid mapping to chromosome 7 (Cosmid 3 - Contig 12), genomic survey sequence.
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Archosauria; Aves; Neognathae; Galliformes; Phaslanidae;
Phasianinae; Gallus.
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Submitted (14-JUN-1999) Law A.S., Division of Molecular Biology,
Roslin Institute, Roslin, Midlothian EH25 9PS, Scotland, UK
                                                                                                                                                                                                                                                                                                                                                                                                                      363 TTGAGGAGCCACAGAGTTGTATAAATTTGTTTAATGATATCCTGCCCTGCCTTCCAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 TCCTGTGGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGGAT 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543 GACAGTGGTACAGGAGCTCTGAATTTTTAGATAAACTATGAGAGTGGAAACAGAATCT 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     597 KKGKKKTKKKGKKKDKKTDDTDDDWWWWTWWATAGWATTGGAAAGGGAATTGAAAAGGWT 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603 GAGGCTAGTTTCTTGAGCTGACTGTAAATTTTGTGAGAATATTTTCAAGACTACATTAGT 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537 AWTGTTTGAWTTTTTTGTGGANAGAATATTTTKGTWTDATWTATATTATTNNTNTTCTCT 478
                                                                                                                                                                                                                                                                                                                                                                 775 KKGWKTWTTWAAWTWDKWTKAWAAWRDAATRTWTDTAAGKKKKKTKKWAATWGATKAKWA 716
                                                                                                                                                                                                                                                               Gaps
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Integration of the genetic and physical maps of the chicken
                                                                                                                                                                                                        Length 919;
                                                                                                        226 others
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               663 TGTGTGTTTGAGGAAAATAAAATGTTTAAGTTGTCCATT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 TTNGTWTTAACGCCATAMTTAATNNAGNATGTCCGCAAAT 438
                                                                                                                                                                                                                                Best Local Similarity 32.4%; Pred. No. 21;
Matches 110; Conservative 77; Mismatches 151;
                                                                                                                                                                                                           DB 12;
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                                                                                                                                                                                                        7.7%; Score 55.4; 1
32.4%; Pred. No. 21;
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/db_xref="taxon:9031"
/chromosome="7"
/map="7q"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR12F23"
                                                                                                     93 9
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GSS; genome survey sequence.
chicken.
                                                                            /note="end : T7"
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                                                                                                     124 c
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7.6%; Score 55; DB 12; Length 411;

Query Match

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                                                                                                                                                                                                                                        Drosophila melanogaster genome survey sequence SP6 end of BAC BACNO3604 of DrosBAC library from Drosophila melanogaster (fruit AL098379 GI:5609990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etded un Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                         ITGAAACTGACTTTCATTTGCAACATGAGAATTGCTGTATTTGT---CAGGTTACAAGTA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 GTGCAATGGCTGCTTAGAAGTAGTGAGAAACATTTAGGGAAATACTGGAGTGAAGCAAAC 330
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                                                                                                                       74 GTCAAAAGTIGGACTCGATGATCTCAGAGTTTTTTCCAGCCTTAATAATTCTATGAAT 132
                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
                       Gaps
                                                       TTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGACAAGGTGATGGTTG 73
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    /organism="Drosophila melanogaster"
/plasmid="pBeloBaC11"
    /db_xref="taxon:7227"
    /clone_lib="DrosBAC"

                      40;
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                    0; Mismatches
     Pred. No. 38;
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66.48;
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                                                                                          631 TITIGIGAGAATATITICAAGACTACATTAGTIGIGIGITIGAGGA 676
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			υ		υ	O		,	o u				e.	RES	9.3	S,	E	DE	X XX	SOS	Nd	X Q	XX PF	PR	A A A	PI	DR.	FT XX
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: August 2, 2002, 13:35:09; Search time 1205.34 Seconds (without alignments) (without alignments) 1029, 858 Million cell undates/sec	ACCTCCCGACCGC	able: II Ga	Searched: 1736436 seqs, 858457221 residues	Total number of hits satisfying chosen parameters: 3472872	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100%	LISCING LIEST 45 SUMMARIES	Database: N_Geneseq_032802:* 1: /SIDSJ/gegdata/hold-geneseq/geneseqn-embl/NA1980.DAT:* 2: /SIDSJ/decdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*	<pre>3: /SIDSI/gcgdata/hold-geneseq/geneseqn embl/NN1982.DAT:* 4</pre>	/SIDS1/gcgdata/hold-geneseq/gene/SIDS1/gcgdata/hold-geneseq/gene	/SIDS1/gcgdata/hold-geneseq/gene /SIDS1/gcgdata/hold-geneseq/gene : /SIDS1/gcgdata/hold-geneseq/gen	: /SIDS1/gcgdata/hold-geneseg/gen : /SIDS1/gcgdata/hold-geneseg/gen : /SIDS1/gcgdata/hold-geneseg/gen	/SIDS1/gcgdata/hold-geneseg/gen	/SIDSI/gcgdata/hold-geneseq/ge	. .	/SIDS1/gcgdata/hold-geneseq/ge: /SIDS1/gcgdata/hold-geneseq/ge: /SIDS1/gcgdata/hold-geneseq/ge	SIDS1/gcgdata/hold-geneseq/gen SIDS1/gcgdata/hold-geneseq/gen SIDS1/gcgdata/hold-geneseq/gen	war bototherd	iter than or equal to the score of the	derived by analysis of the total score di	SUMMARIES * SUMMARIES **	No. Score Match Length DB ID Description	723 100.0 723 54.8 7.6 12007	51.2 7.1 18585 24 ABL34609 Humon 49.8 6.9 7669 22 AAS46597 Thumon 7	49.8 6.9 7669 24 ABL33846 48.2 6.7 14147 22 AASAG744	411 22 AAI81186 17738 24 ABL33538 6419 24 ABL32267

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                                                                                       putative exón was isolated of a gene that was designated CHD-W due to its close identity to the mouse CHD-1 gene and its W location. This CHD-W fragment was used to isolate a similar gene (see also AAT4751) from chicken. This gene was not W-located, and was named to CHD-1A. A second, W-located chicken gene (CHD-W) closely related to CHD-1A was also identified (see also AAT42754). The CHD-1A and CHD-W genes are useful for bird sex determn.
                                                  derived from great tit. It represents part of an intron in ted gene. By moving downstream from this sequence, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCCAATGGCTGCTTAGAAGTAGTGAAAA
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                                                                                                                                                                                                                                                                                                  Length 723;
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                                                                                                                                                                                                                                              Sequence 723 BP; 188 A; 109 C; 164 G; 262 T; 0 other;
                                  GT-W (AAT42755) was cloned from a W chromosome
                                                                                                                                                                                                                                                                                                100.0%; Score 723; DB 18;
11arity 100.0%; Pred. No. 1.3e-152;
Conservative 0; Mismatches 0;
8; Fig 1; 76pp; English.
                                                                                                                                                                                                                                                                                                                    Similarity
                                                        product derived f
a W-linked gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 TITITITICCAGCCTTAATAATICTATGAATICTGTAATITITATICTTGATCTTTTTGAGC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful
                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic; antianeamic; oytostatic; nootropic; nontianeamic; neuroprotective; anti-HV; anticonvulsant; ophthalmologici; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anamia, acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; Inhumatoid arthritis; psoriasis; bowel disease;
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nent of diseases associated with
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ches 202;
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                                                               ID NO:
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46.6%; Pred. No. 0.0
                                                               Human immune system associated gene SEQ
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2000DE-1043826
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                                 entry)
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Best Local Similarity 46.6
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leic acid comprising diagnosis and treatm
                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytosine methylation
                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-130909/17
                                                                                                                                                                                                                                                                     WO200200928-A2
                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid
                               26-MAR-2002
                                                                                                                                                                                                           gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8985
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AAS46597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human metastasis associated genes which are modified by cytosine methylation. The sequences can be used in the diagnosis and treatment of cancer. The present sequence is one of the genes of the invention.
               103 TITITITICCAGCCTTAATAATICTATGAATTCTGTAATTTTATTCTTGATCTTTTTGAGC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 GAAGTITGTTTGGGGAITTTAGTTTGGTTTCCCTGTCACTGTTTTCTTTCCTTGAAACTG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 ACTITCATITGCAACATGAGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCAATGGCTG 282
343 CCAAACTGTAGCTTTGGGATTTGAGGAGCCACAGAGTTGTATATAATTTGTTTAATGAT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid derived from chemically treated metastasis genes, useful for diagnosis of cancers by analysis of cytosine methylation, also for treatment
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7.1%; Score 51.2; DB 24; Length 18585;
Best Local Similarity 43.4%; Pred. WO. 0.046;
Matches 256; Conservative 0; Mismatches 308; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                       Metastasis associated gene; cytostatic; gene therapy; cancer; cytosine methylation; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 162; 23pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                        Human metastasis associated gene SEQ ID NO: 162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olek A, Piepenbrock C, Berlin K;
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                                                                                                                                                              9345 ttttttttgtatttta 9362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2001; 2001WO-EP03970.
                                                                                                                                 463 TTTTTTTGGCTTCTTCA 480
                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
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Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
15671 atttaatttaaggatatttttttttttattataagataaagtttagattitttaaagtag 15730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                        463 TTTTTTTTGGCTTCTTCATATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCA 522
                                                                                               283 CTTAGAAGTAGTGAGAAACATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTG 342
                                                                                                                                                                                                                   343 CCAAACTGTAGCTTTGGGATTTGAGGAGCCACAGAGTTGTATAAATTTGTTTAATGAT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 GAACTAGGAGATCTGTGGATGACAGTGGTACAGGAGCTCTGAATTTTTTAGATAAACTAT 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583 GAGAGTGGAAACAGAAATCTGAGGCTAGTTTCTTGAGCTGACTGTAAATTTTGTGAGAAT 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour suppressor gene derived chemically modified sequence #319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS46597 standard; DNA; 7669 BP.
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07-APR-2000, 2000DE-1019173.
30-JUN-2000, 2000DE-1035529.
01-SEP-2000, 2000DE-1043826.
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and concogenes having a sequence taken from 550 actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (SS) and sequences complementary to (SS). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may for analysing diseases for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to parients. The present sequence is one of the constant of the diagnosis and for an edisadvantageous to parients. The present sequence is one of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 ATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCCCTGCCTTCC 420
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                                                                                                                                                                                                                                                                                                                                                                                 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7669;
                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7669 BP; 1788 A; 168 C; 1959 G; 3754 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49.8; DB 22;
Pred. No. 0.079;
0; Mismatches 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2546 gittaagigatittigagittitagittittaag 2578
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Best Local Similarity
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The present invention provides a number of human immune system associated denses which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reluxaemia, Alzheimer's disease, Alzheimer's disease, Alzheimes's incurrent in eurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                   antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCAATGGCTGCTTAGAAGTAGTGAGAAA
                                     antiasthmatic;
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for diagnosis and treatment of diseases associated with abnormal
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                                     Human; immune system disease; cytosine methylation;
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44.4%; Pred. No. 0.079;
Live 0; Mismatches 252;
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01-SEP-2000; 2000DE-1043826.
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Human immune system associated gene SEQ ID NO: 1819.

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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DRA (CP DNA) e.g. with bisulphite, of a segment of chemically pretreated DRA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (CS) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may compared a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for accertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific compared to another set of genetic and/or epigenetic and/or prognosis events which are disadvantageous to patients. The present sequence is one of the care disadvantageous to patients. The present sequence is one of the compared to another set of genetic and/or prognosis and/or prognosis events with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. 12 and 1D). ID 536 and ID 535, except for those whose partner sequence is missing).

Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                            Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
cytosine methylation; ds.
481 TATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGG 540
                                                                                                                                                                                                                                                                                                                                                                                   Tumour suppressor gene derived chemically modified sequence #468.
                                                                                                                2546 gtttaagtgattttgagtttttaag 2578
                                                                                      541 ATGACAGTGGTACAGGAGCTCTGAATTTTTAG 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 468; 27pp; English.
                                                                                                                                                                                                                                              AAS46744 standard; DNA; 14147 BP.
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07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-103559.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                          (first entry)
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AA013910) that exhibit activity elating to
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                                                                                                                                                                                                                                                                        2917 tgcggatatagtcgagaacgtaatagataataattatttgttttagaggagtttatatttt 2976
                                                                                                                                                                                                                                                                                                                                                                                                                             2977 agtaggaaaggtagatgagaaaaaaggtaaatatgtataagagtgcgttagatggtggta 3036
                                                                                                                                                                                                       569 TTTAGATAAACTATGAGAGTGGAAACAGAAATCTGAGGCTAGTTTCTTGAGCTGACTGTA 628
                                                                                                                                                                                                                                                         449 TTTTTTTTTTTTTTTTTTTTTTGGCTTCTTCATATCCTGTGGTAATGAGTTAATGCATTT 508
                                                                                                                                                                                                                                                                                                                          509 AGAAGCACATGGCAGAACTAGGAGATCTGTGGATGACAGTGGTACAGGAGCTCTGAATTT 568
                                                                                                                                                                                   389 ATTIGITIAATGATATCCTGCCCCTGCCTTCCATTAATTGCTTGTTTAATGAAACCACTC 448
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing isonosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                  Length 14147;
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of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                   Sequence 14147 BP; 3856 A; 225 C; 3554 G; 6512 T; 0 other;
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    629 AATTTTGTGAGAATATTTTCAAGACTACATTAGTTGTGTTTTGA 673
                                                                                                                  Ouery Match 6.7%; Score 48.2; DB 22; Best Local Similarity 48.1%; Pred. No. 0.2; Matches 137; Conservative 0; Manatches 148;
                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polynucleotide SEQ ID NO 1246.
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18-MAY-2000; 2000US-0577409.
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P-PSDB; AAO01255.
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AAI81186/c
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Claim 1; SEQ ID NO 1511; 32pp + Sequence Listing; German.
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oytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiseis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 TATAAATTTGTTTAATGATATCCTGCCCTGCCTTCCATTAATTGCTTGTTTATGAAAC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 CACTCTTTTTTTTTTTTTTTTTTTTTTTTTGGCTTCTTCATATCCTGTGGTAATGAGTTAATG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 22; Length 411;
Pred. No. 0.11;
0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                             Sequence 411 BP; 160 A; 30 C; 75 G; 40 T; 106 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
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2000DE-1043826
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01-SEP-2000;
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Local Sim.
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rhemmatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564 AATTTTTAGATAAACTATGAGAGTGGAAACAGAAATCTGAGGCTAGTTTCTTGAGCTGA 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      624 CTGTAAATTTTGTGAGAATATTTTCAAGACTACATTAGTTGTGTGTTTGAGGAAAATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                          6.5%; Score 47.2; DB 24; 59.8%; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         684 AATGTTTAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200200928-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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us-08-973-363-1.rng

01-SEP-2000; 2000DE-1043826

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer, s disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatoryulecrative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 ITTTTTTCCAGCCTTAATAATTCTATGAATTCTGTAATTTTAATTCTTGATCTTTTTGAGC 162
                                                                                                                                                                                                                                                                                                                                                                                        163 GAAGITIGITIGGGGAITITAGIIIGGIIICCCIGICACIGIITICITICCTIGAAACIG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 ACTITCATITGCAACAIGAGAATIGCTGTATTIGTCAGGTTACAAGTGCAATGGCTG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 CTTAGAAGTAGTGAGAAACATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 CCAAACTGTAGCTTTGGGATTTGAGGAGCCACAGAGTTGTATAAATTTGTTTAATGAT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic; antiateriostotic; antianemic; cytostatic; nootropic; noetropic; antienteriostatic; anti-HTV; anticonvulsant; obthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antifilammatory; cancer; eye disease; arterioscierosis; anemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                   6.5%; Score 47; DB 24; Length 6419;
44.7%; Pred. No. 0.32;
tive 0; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1831 ttatttttgtatttatttatttattttttttttttatttatttattta 1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          463 TITITITIGGCTTCTTCATATCCTGTGGTAATGAGTTAATGCATTTA 509
                                                                                                                                                                           Sequence 6419 BP; 1565 A; 53 C; 1453 G; 3348 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 1201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL33228 standard; DNA; 6861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-2001; 2001WO-EP07537.
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                                                                                                                                                                                                                                                                         Matches 182; Conservative
                                                                                                                                                                                                                                                     Local Similarity
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30-JUN-2000; 2000DE-1032529.

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelold leukaemia, Albahemer, Albahemer, Albahemer, Albahemer, adisease, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 TIGGGATTTGAGGAGCCACAGAGTTGTATAAATTTGTTTAATGATATCCTGCCCTGC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 ttaggaattatggataaaaatatatataaatttatatatatattaatattaattattatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 CTTCATATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          537 atttattttatgttgtatatattttttttatagtaaaagagaaggaaatgatttatagttt 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic; antiatrerioscelerotic; antianemic; cytostatic; nootropic; noetropic; entiatrerioscelerotic; antianemic; cytostatic; nootropic; antiinteumatic; antiarthritic; antidiabetic; antipsoriatic; antifilfammatory; cancer; eye disease; arteriosclerosis; anemia; acute myeloid leukaemia; Alzhehmer's disease; AIDS; epilepsy; neurofibromatosis; hewmatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.5%; Score 47; DB 24; Length 6861; 50.7%; Pred. No. 0.33; tive 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6861 BP; 1740 A; 246 C; 1607 G; 3268 T; 0 other;
                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1201; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536 TGTGGATGACAGTGGTACAGGAGCTCTGAATTTTTAGATAAA 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           597 tatatagtattttggagagatagttatgaaaattgttaagaaa 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 299.
                                                                              Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL32326 standard; DNA; 6109 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 113; Conservative
                                                                            Piepenbrock C,
                                      (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                   for diagnosis and tre
cytosine methylation
                                                                                                                     WPI; 2002-130909/17
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Best Local Similarity
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                                                                                 Olek A,
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reluxenmia, Alzheimer's disease, Alzheipsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 TTTGGGATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCCCCTG 414
                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTCATATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595 AGAAATCTGAGGCTAGTTTCTTGAGCTGAAAATTTTGTGAGAATATTTTCAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 CTGTGGATGACAGTGGTACAGGAGCTCTGAATTTTTTAGATAAACTATGAGAGTGGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            655 ACATTAGTTGTGTTTGAGGAAAATAAAATGTTTAAGTTGTCCATTCCTTGA 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.5%; Score 46.8; DB 24; Length 6109; 45.8%; Pred. No. 0.36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6109 BP; 1232 A; 195 C; 1734 G; 2944 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 192; Indels
                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 299; 32pp + Sequence Listing; German.
                                                                                                       Berlin K;
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              2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                     Piepenbrock C,
                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                              cytosine methylation
                                                                                                                                        WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
              30-JUN-2000;
01-SEP-2000;
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                                                                                                       olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the chemical pretreatment converts cytosine bases unmethylated at the dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by anabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac asthma, HDR syndrome, Saethne-Chotzen syndrome, renal disease, sthma, HDR syndrome, Saethne-Chotzen syndrome, renal disease, preclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene requiation-associated genes.
nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 TITIGGGATTTGAGGAGCCCACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCCCCTG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       535 CTGTGGATGACAGTGGTACAGGAGCTCTGAATTTTTAGATAAACTATGAGAGTGGAAAC 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6109 BP; 1232 A; 195 C; 1734 G; 2944 T; 4 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 33; 26pp; English.
                                                                                                                                                                                                                                                                                                                                           Berlin K;
                                                                                                                                                                                                                  2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                            06-APR-2001; 2001WO-EP03968
                                                                                                                                                                                                                                                                                                                                           Piepenbrock C,
                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG
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                                                                             WO200177375-A2
                                       Homo sapiens
                                                                                                                                                                                                                    07-APR-2000;
30-JUN-2000;
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer, disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention. 595 AGAAATCTGAGGCTAGTTTCTTGAGCTGACTGTAAATTTTGTGAGAATATTTTCAAGACT 654 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation Human; immune system disease; cytosine methylation; antiasthmatic; antiateriosocalerotic; antianemic; cytostatic; nootropic; neuroprotective; anti-HTV; anticonvulsant; ophthalmologica; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosocierosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; ALDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; 655 ACATTAGTIGIGITITIGAGGAAAAATAAAATGTTTAAGTIGICCATTCCTTGA 708 Claim 1; SEQ ID NO 288; 32pp + Sequence Listing; German. Human immune system associated gene SEQ ID NO: 288. Olek A, Piepenbrock C, Berlin K; ABL32315 standard; DNA; 6641 BP. 30-JUN-2000; 2000DE-1032529. 02-JUL-2001; 2001WO-EP07537. 26-MAR-2002 (first entry) (EPIG-) EPIGENOMICS AG. WPI; 2002-130909/17. WO200200928-A2. Homo sapiens. 03-JAN-2002. ABL32315; gene; ds. ABL32315 ò

The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention. WO200200928-A2. Homo sapiens. 2366 tt 2367 03-JAN-2002. 463 TT 464 tene; ds. RESULT 14 ABL33013 g δ g ò Q δ 103 ITITITICCAGCCTIAATAATICTATGAATICTGIAATTTTATTCTTGATCTTTTTGAGC 162 163 GAAGITIGITIGGGGATTTTAGTTTGGTTTCCCTGTCACTGTTTTCTTTCCTTGAAACTG 222 0; Gaps 6.5%; Score 46.8; DB 24; Length 6641; 45.6%; Pred. No. 0.36; tive 0; Mismatches 197; Indels 0; Sequence 6641 BP; 2495 A; 22 C; 984 G; 3140 T; 0 other; = Conservative Query Match Best Local Similarity Matches 165;

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2126 atttaattgtgttaattaattaatttttgtttaaaatgtttaaagtgtttaatttgttt 2185 283 CTTAGAAGTAGTGAGAAACATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTG 342 343 CCAAACTGTAGCTTTGGGATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGAT 402 223 ACTITCATITGCAACAIGAGAAITGCTGTATTIGTCAGGITACAAGTAGFGCAATGGCTG 282 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal Human; immune system disease; cytosine methylation; antiasthmatic; antiateriosolerotic; antianemic; cytostatic; nootropic, noetropic, noetropic, anti-HTV; anticonvulsant; ophthalmologica; antirheumatic; antiathritic; antidiabetic; antipsoriatic; antilfiammatory; cancer; eye disease; arteriosolerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; ALDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; Claim 1; SEQ ID NO 986; 32pp + Sequence Listing; German. Human immune system associated gene SEQ ID NO: 986. Berlin K; ABL33013 standard; DNA; 7597 BP. 02-JUL-2001; 2001WO-EP07537. 30-JUN-2000; 2000DE-1032529. 01-SEP-2000; 2000DE-1043826. 26-MAR-2002 (first entry) Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG. for diagnosis and tre cytosine methylation WPI; 2002-130909/17 á

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Claim 1; SEQ ID NO 1732; 32pp + Sequence Listing; German.
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                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                            475 TCTTCATATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGAT
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0
                                                                 Length 7597;
                Sequence 7597 BP; 1965 A; 109 C; 1790 G; 3733 T; 0 other;
                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune system associated gene SEQ ID NO: 1732
                                                                   DB 24;
                                                                                                   0; Mismatches 192;
                                                                 Score 46.8; DB Pred. No. 0.37;
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2000DE-1043826
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                                                                                   Best Local Similarity
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                                                                 Query Match
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 TTGTATATAAATTTGTTTAATGATATCCTGCCCCTGCCTTCCATTAATTGCTTGTTTAT 438
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Pred. No. 0.41;
0; Mismatches 169;
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ne: 25768 sec
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Matches 159; Conserv
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AS8683 Sequence 4
A58685 Sequence 4
A58686 Sequence 3
L10410 Nouse DNA-b
A58684 Sequence 3
L10410 Nouse DNA-b
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unidentified
unclassified
1 (bases 1 to 153)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
BIRDS
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224
Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
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Sequence 2 from Patent WO9639505.
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AUTHORS
TITLE
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FEATURES
                                                                                                                                                                             August 2, 2002, 20:28:20; Search time 12674 Seconds (without alignments) 252.625 Million cell updates/sec
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153
1 AITCITCCAGAIGAICCTGA.......CICAGAGACITIGIGGIGCG 153
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                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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gb_p1:*
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                                                                                                                                61 CAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTT 120
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Pred. No. 3.5e-19;
0; Mismatches 29;
                    100.0%; Score 153; DB 6;
100.0%; Pred. No. 2.6e-32;
ive 0; Mismatches 0;
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
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    153
    /organism="unidentified"
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Sequence 5 from Patent W09639505.
A58686
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Griffiths, R. and Tiwari, B.
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Griffiths, R. and Tiwari, B.
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Best Local Similarity 80.9%;
Matches 123; Conservative
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
BIRDS
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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Pred. No. 3.5e-19;
0; Mismatches 29;
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                                Patent: WO 9639505-A 5 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224
Location/Qualifiers
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224
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                                                                                                                           /organism="unidentified"
/db_xref="taxon:32644"
34 c 31 g 28
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/db_xref="taxon:32644"
10 c 31 g 20
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Sequence 3 from Patent W09639505.
A58684
A58684.1 GI:3714247
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Best Local Similarity 80.9%;
Matches 123; Conservative
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/ Product = "DNA - DI Inding protein"

/ Product = "DNA - DI Inding protein"

/ Protein_1 = "AABOG 486 1."

/ Protein_1 = "Inding protein"

/ Protein_1 = "Inding p
                                                                                                                                                                                         Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. (Dassa 1 to 5149)
Delmas, V. Stokes, D.G., and Perry, R. P. A mammalian DNA-binding protein that contains a chromodomain and an SNR2/SWIZ-like helicase domain
Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
                          ROD 19-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 5349)
Perry, R.P.
Direct Submission
Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, Pa 19111, USA
On Feb 16, 1994 this sequence version replaced gi:293322.
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                   MUSCHDIX 5349 bp mRNA linear RV wouse DNA-binding protein (CHD-1) mRNA, complete cds. L10410. X66028 L10410.1 GI:455014 DNA binding protein. Mus musculus
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1067 c 1319 q 1224 t
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1. 5349
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171. 5306
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/gene="CHD-1"
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Gaps

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RLDA TARDAELVDKSETDLRRLGELVHNGCTKALKDSSSGTERTGGRLGKVKGPTFRI
SGYQVAKLYTSHEEELTPLHKSIPSDPEERKQYTIPCHTKAAHFDIDWGKEDDSNLL
IGIYEYGYGSWEMIKMDPLOLTHKILPDDPDKRPOAKOLQTRADYLIKLLSRDLAKK
BALSGAGSSKRRRARAKKNAMKSIKVKEETKSDSSPLPSEKSDBDDDKLSESKSUGR
ERRKSSVSDAPVHTTASGEPVPISEESKEELDQYTFSICKERNRPVKAALKQLDRPEK
GLSRFREQLEHTRQCLIKTGHTTECLKEYTNPPQIKQMRKNLMIFVSKFTEDDARKLH
KIYKHAIKKOEDSGOANSDONSUNAPHYTRNPDYBELKENTHIDDSSRDSYSSDRHLTO
YHDHHKDRHQGDSYKKSDSRKRPYSFSNGKDHRDWDHYKQDSRYYSDREKHELDDH
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Submitted (03-JUN-1997) Laboratory of Gene Transfer, National Human
Submitted (03-JUN-1997) Laboratory of Gene Transfer, National Human
Genome Research Institute, National Institutes of Health, 49
Convent Drive, Bethesda, MD 20892-4442, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (basea I to 5947)
Woodage_T., Basrai_M.A., Baxevanis,A.D., Hieter,P. and Collins,F.S. Characterization of the CHD family of proteins
Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
                                                                                                                                                                                                                            linear PRI 27-NOV-1997
                       52 AAAAAACCACAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGC 111
                                                                                                      112 AGAGATCTTGCAAAAAGAGGCTCAGAGACTTTGTGGTGCG 153
                                                                                                                                                                                                           Homo sapiens CHD1 mRNA, complete cds.
AF006513.1 GI:2645428
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/db_xref="taxon:9606"
/chromosome="5"
/map="5q15-21; near WI-5811"
1. .5947
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/protein_id="AABB7381.1"
/db_xref="GI:2645429"
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164. .5293
/gene="CHD1"
/codon_start=1
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Woodage, T.
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26851 AGAGATCTTGCAAAAAAAGAAGTC 26827
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

On Dec 7, 2001 this sequence version replaced gi:15290448.

On Dec 7, 2001 this sequence version replaced gi:15290448.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.sigc.stanford.edu

Quality: Phrap Quality >=40 100% of Sequence;

Estimated Total Number of Errors is 0.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624.

The number of bases overlapped is 90404.
RSRDHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSSEYTHHKSSRDYRYHSDWQMDH
RASSSGPRSPLDQRSYGSRSPFEHSVEHKSTPEHTWSSRKT"
1004 c 1243 g 1570 t
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
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DOE Joint Genome Institute.
Dorect Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Pred. No. 2.7e-11;
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34122 a 18862 c 17827 g 30409
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/db_xref="taxon:9606"
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Homo sapiens clone RPl1-58M12, WORKING DRAFT SEQUENCE, 10 unordered
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2 (bases 1 to 134365)

DOE Joint Genome Institute.

Direct Submission

Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Birren, B.; Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-58M12
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Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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AC012624 134365 bp DNA linear PRI 21-JUL-;
Homo sapiens chromosome 5 clone CTD-2082117, complete sequence.
AC012624
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40414 a 24497 c 25503 g 43951
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/db_xref="taxon:9606"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Center project Information

Center project name: 15134

Center project name: 58_M_12

Center project name: 58_M_12

Sequencing vector: MI3; MI7815; 100% of reads

Absembly program: Phrap, version of 560731

Absembly program: Phrap, version of 560731

Consensus quality: 134743 bases at least Q40

Consensus quality: 134227 bases at least Q30

Consensus quality: 134227 bases at least Q30

Consensus quality: 140814 bases at least Q20

Insert size: 144000; agarose-fp

Insert size: 144000; agarose-fp

Cuality coverage: 4.6 in Q20 bases; sum-of-contigs
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ACUUBS31 145659 bp DNA linear HTG 14-FEB-2001 Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE, Acrossing pieces.
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA
On Feb 14, 2001 this sequence version replaced gi:7528342.

-----Genome Center
Center: Joint Genome Institute
Center: Joint Genome Institute
Center Code JGI
Web site: http://www.jgi.doe.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="RPCI-11 Human Male BAC"
1. .38820
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Anote= assembly_tragment.
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/note="assembly_fragment"
40512. 43279
/note="assembly_fragment"
                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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1 (bases 1 to 145659)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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HTG; HTGS_PHASE2; HTGS_DRAFT.
Location/Qualifiers
1. .143079
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2 (bases 1 to 145659)
DOE Joint Genome Institute.
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ORIGIN
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Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Geome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA -----Genome Center Joint Geome Institute
                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q30
Consensus quality: 184175 bases at least Q30
Consensus quality: 184175 bases at least Q30
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of unknown length
contig of 1209 bp in length
gap of unknown length
contig of 1956 bp in length
gap of unknown length
contig of 1997 bp in length
contig of 1975 bp in length
gap of unknown length
contig of 1502 bp in length
gap of unknown length
contig of 1502 bp in length
gap of unknown length
contig of 1064 bp in length
contig of 2100 bp in length
gap of unknown length
contig of 1670 bp in length
gap of unknown length
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of 3948 bp in length
unknown length
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of 4978 bp in length
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of 4585 bp in length
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contig of 4813 bp in length
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Sequencing of Human Chromosome 5
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Center clone name: RPCI-11_36012
                                                                                                                                                                                                                           Web site: http://www.jgi.doe.gov
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                                           2 (bases 1 to 193446)
DOE Joint Genome Institute.
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                                                                                     Direct Submission
                                                                                                                                                                                                  Center Code: JGI
                    Unpublished
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                                           REFERENCE
AUTHORS
                                                                                       TITLE
                         JOURNAL
  TITLE
                                                                                                                                                           COMMENT
                                                                                                                        Consensus quality: 139128 bases at least 040
Consensus quality: 14556 bases at least 030
Consensus quality: 14374 bases at least 030
Consensus quality: 14374 bases at least 030
Consensus quality: 14374 bases at least 030
Estimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.27 in 020 bases; pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. Gaps between the contigs estimation.

* some sent of a runs of N. The order of the pleces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have.

* This sequence will be replaced
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AC091946.1 GI:14333882
HTGS_PHASE1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 193446)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ** by the finished sequence as soon as it is available and the accession number will be preserved.

** 56178: contig of 56174 bp in length 56178: 56274: gap of unknown length 56275 100874: gap of unknown length 100875 110974: gap of unknown length 113227: contig of 12133 bp in length 113228 113227: contig of 12133 bp in length 11329 113290: gap of unknown length 11329 113990: gap of unknown length 118291 118291 119694: contig of 1404 bp in length 118291 119694: contig of 1404 bp in length 119695 123297: contig of 3503 bp in length 119695 123397: gap of unknown length 119698: contig of 3503 bp in length 113398 123397: gap of unknown length 113398 113398 123397: gap of unknown length
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26309 c 27580 g 48609 t 600 others
                                         Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .145659
/organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .145659
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/clone="CTC-480B11"
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                         Project Information
                                                                                                               Summary Statistics
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Matches 80; Conserv
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ACU92382 276181 bp DNA linear HTG 03-JUL-2001 Homo sapiens chromosome 5 clone RP11-75H1, WORKING DRAFT SEQUENCE, 47 unordered pieces.
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                                           Direct Submission
Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 89429 AAAAAACCACAAGCAAAAACAGTTGCAGACCCGTGCAGACTACCTCATCAAATTACTTAGT 89370
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       4 (bases 1 to 219250) DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 219258;
                                                                                                                                             www.jgi.doe.gov
Prinshing Completed at Stanford Human Genome Center
www.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
STS Content:
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HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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Consensus quality: 229677 bases at least Q40
Consensus quality: 256163 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="crb-2007H13"
71954 a 42062 c 40933 g 64309 t
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Web site: http://www.jgi.doe.gov
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DOE Joint Genome Institute.
Direct Submission
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SHGC-103595 G57841.
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WI-13675 G23101
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Matches 80; Conserva
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Due Joint Genome Institute.

Due Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 219258)

Direct Submission

Does Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (11-A00-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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1 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
Unpublished
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Homo sapiens chròmosome 5 clone CTD-2007H13, complete sequence.
AC022121
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                                                                                                                                                                                                                                                                                      gap of unknown length
contig of 6675 bp in length
gap of unknown length
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/clone_lib="RPCI human BAC library 11"
57571 a 35252 c 37061 g 60360 t 3202 others
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/db_xref="taxon:9606"
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Matches 80; Conservative
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A58691
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     Estimated insert size: 174820; agarose-fp estimation
Estimated insert size: 174820; agarose-fp estimation
Estimated insert size: 271581; sum-of-contigs estimation
Guality coverage: 8.62 in Q20 bases; agarose-fp estimation
Quality coverage: 5.5 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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quality: 260799 bases at least Q20
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Griffiths, R. and Tiwari, B.
BIRDS
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Db 213673 AAAAAACCACAAGCAAAACAGTTGCAGACCCGTGCAGACTACCTCATCAAATTACTTAGT 213614
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51769 c 50026 g 82854 t 4673 others
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ISIS INNOVATION (GB)
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A58691
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COMMENT Other publication AU 5906996 961224.
FEATURES Location/Qualifiers
1. .6608
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/db_xref="taxon:32644"

BASE COUNT 2289 a 1207 c 1459 g 1653 t
ORIGIN

Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
Griffiths, and Korn, R.M.
A CHDI gene is Z chromosome linked in the chicken Gallus domesticus
Gene 197 (1-2), 225-229 (1997) 2 (bases 1 to 6872)
Griffiths, R. and Korn, R.M.
Direct Submission
Submitted (Gr-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 8QQ, UK VRT 08-OCT-1997 'product="chromo-helicase-DNA-binding on the Z chromosome /gene="CHD-2" 228. .5654 /gene="CHD-2" /function="role in chromatin architecture" /note="CHD protein with hydrophilic domain" /codon_start=1 1. .6872 /organism="Gallus gallus" /db_xref="taxon:9031" 1. .6872 .ocation/Qualifiers AF004397.1 GI:2501845 AF004397 ORGANISM REFERENCE AUTHORS ACCESSION gene JOURNAL AUTHORS JOURNAL MEDLINE REFERENCE KEYWORDS FEATURES

LKCONVKGMIKLDNYKKDOETKRWLKNASPEDVEYYYCOTHNWONININININIELL AHSWKSSAGYPDYYCKWOCLPYSECSWEDOLIAKKFOALIDEYSENGSKTPPRD CKVLKQRPRYPAKKQPSYTGGHESLELRYOLUNIMILAHSWCKGNSCTLADEBGLG KTUQT ISFLNYLFHENQLYGPFLLRYPLTSWQRETOTWAPOMNAVYYLGDTYSR MIRTHEWHHPOTKREK MILLTYPETLLKKSFLGGLWNAFICVDBAPURKNDDSLLY MILTHEWHLLTYTPLQNSLKELWSLLHTIMPEKFSSWEDFEEBIGKOREKYYN

SQSGSDSESGSESGSESESDTSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAV LKKQQQQCKAASDSGSEEDSSSSEDSADDSSSETKKKKKKKKBDWQMSGSGSVSGTGS DSESAEDGOKSSCEESESDYEPKNKVKRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE DDDEDYZKRGRYGATYNVNYYKPEETKTDSDDLLEVCGEDDYPQTEEDEFETIEKEMD SRIGKKGARGASTTIYAVEADGDDAAGFEKSKELGELQILIKWGWSHIHKTWET

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PLESTRAGGLGINIAASADTVYLTDSDNAPOWLDGAQARAHTGGKKOWLDTRYKTGS
VEDDILERAKKWALDHLVIORANDTGKYVLHTGSTPSSPPRWEELSALKKGAEE
LEYREPGESEGEPOWDD DED IKKARETRENEPGFLYCOELLSGFKWARTSHDEDDIE
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QVNAKLVISHBEELAPLEKSTPSDEPERKRYVTPCHTKAAHTDIDNGKEDDSHLLVGT
YEYGYGGEBLANDLAGTOKTHONGTSRAMDTAYLIKLLANDLAKKEA
RAGAGGAGSRATTRAKTRAKTRAKTRAKTRYTENETRESKRYTERERESKRYTERATSHOPPORKEESTATTATSEPPYTSE
BSEELHGKTFSCYGERVEREKYNDMKSTRAKTRKKTROTATTSTEPYPISE
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/note="short insert found in longer variant mRNA of CHD-2" ORIGIN

Query Match 44.7%; Score 68.4; DB 5; Length 6872; Best Local Similarity 79.4%; Pred. No. 6.4e-09; Matches 81; Conservative 0; Mismatches 21; Indels 0; Gaps

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OY 51 CARARACCAGGARACAGGTTACAGCCGGTGCAGCTTACCTACTTAGGTTG 110
Db 4100 CARGAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGCTACCTCATTAAATTACTGAA 4159

Search completed: August 2, 2002, 20:29:35 Job time: 25016 sec

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Title: Perfect score: Sequence:

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Run on:

Scoring table:

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Database :

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ABA246384
ABA165871
ABA165871
ABL52834
ABB122834
AAX61176
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AAX61776
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AAX6636
AAX6636 Location/Qualifiers 52..81 /*tag= a /note= "bases 52-81.a Mouse CHD-1 gene (bases 3855-977). BP. AAT42756 standard; DNA; 153 24.4 6118
22.1 5649
22.2 9 64813
22.2 9 64813
22.2 6 2813
22.2 6 2813
22.4 847 2
22.4 847 2
22.4 847 2
22.4 11244
22.4 11244
22.4 11244
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21.7 13409
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21.7 3409 12-MAR-1997 (first entry) Key misc_difference WO9639505-A1 12-DEC-1996. 3.22.22.24 3.22.22.23 3.22.22.23 3.42.23 AAT42756; Mus sp. AAT42756

IID AAT4

AAC AACA

AAC AACA

AACA N_Genesseq_032802:*

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| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Nkl)99.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Nkl)99.DAT:* Mouse CHD-1 gene (
Great tit CHD-W ge
Chick CHD-W gene f
Chick CHD-1A gene
Chicken CHD-1A gen
Chicken CHD-1A gen
Altered telomere r
Human digestive sy
Human oolorectal c August 2, 2002, 20:44:37; Search time 1205.34 Seconds (without alignments) 217.937 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. US-08-973-363-2 153 1 ATTCTTCCAGATGATCCTGA......CTCCAGAGACTTTGTGGTGCG 153 Description GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd Total number of hits satisfying chosen parameters: 1736436 seqs, 858457221 residues SUMMARIES Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries AAT42756
AAT42759
AAT42758
AAT42751
AAT42751
AAT42751
AAT42754
AAT57603 - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 ü Minimum DB seq length: 0 Maximum DB seq length: 2000000000

(ISIS-) ISIS INNOVATION LTD.

96WO-GB01341 95GB-0011439

05-JUN-1996; 06-JUN-1995;

DB Length

% Query Match

Score

1 153 100.0 1 105.6 69.0 1 105.6 69.0 4 102.4 66.9 6 67.4 44.1 6 67.4 44.1 7 8 41.2 26.9

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61 CAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = AVian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42757), and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAAACAGTTACAGACCAAAAAAACCA 60
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"bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
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                                                                      Avian chromodomain-helicase-DNA binding genes determine sex
                                                                                     - used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                   DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                              Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 70.1%; Score 107.2; DB
81.6%; Pred. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 52..81
                                                                                                                           Claim 8; Fig 3; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chick CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 124; Conservative
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                 WPI; 1997-043127/04.
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                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                    P-PSDB; AAW08149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9639505-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT42758;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                          birds
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                                                                                                                                                                        Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW081464-9. The CHD-IA (see also AAT47251) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 caagcaaaacagttacagacccgtgcagactacctcatcaaactacttagcagagatctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 attettecagatgatectgataaaaaaccacaagcaaaacagttacagaccaaaaaacca 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATTCTTCCAGATGATCCTGATAAAAACCACAAGCAAAACAGACGAGACCAAAAAACCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
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                                                                                       Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                Sequence 153 BP; 61 A; 37 C; 27 G; 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 153; DB 18; 100.0%; Pred. No. 1.8e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT42759 standard; DNA; 153 BP
                                                                                                                                              Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Great tit CHD-W gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-GB01341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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/note=
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В;
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Tiwari
                                  WPI; 1997-043127/04.
P-PSDB; AAW08146.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9639505-A1
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Matches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Bird;

RESULT AAT 427

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Gaps

Indels

Length 153;

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Gaps

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Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT47754) and CHD-W (see also AAT47754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCAACAAACTACTTAGCAGAGATCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The chicken CHD-W gene (AAT42754) acting alone or in conjunction with
                                                                                                                                                                                                                                                                                                                                                                                     1 ATTCTTCCAGATGATCCTGATAAAAACCACAAGCAAAACAGTTACAGACCAAAAAACCA 60
                                                                                                                                                                                                                                                                                                                                                                                                             Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                            Query Match 66.9%; Score 102.4; DB 18; Length 153; Best Local Similarity 79.6%; Pred, No. 4.7e-20; Matches 121; Conservative 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                         Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GCAAAAAGAGGCTCAGAGACTTTGTGGTGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
228..5390
/*tag~ a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT42751 standard; cDNA; 6608 BP
                                                     Claim 8; Fig 3; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chicken CHD-1A gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT42751;
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                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATTCTTCCAGATGATCCTGATAAAAACCACAAGCAAAAACGTTACAGACCAAAAAACCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             a "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
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                                      in
                                                                                                                                                                                                                                                                                                                                                 Query Match 69.0%; Score 105.6; DB 18; Length 153; Best Local Similarity 80.9%; Pred. No. 5.8e-21; Matches 123; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bird; sex determination; chromodomain-Helicase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss.
                                  Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                           Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAAAAAGAGGCTCAGAGACTTTGTGGTGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
52..81
/*tag= a
/note= "bases 52-81 a
                                                                                          Claim 8; Fig 3; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT42757 standard; DNA; 153
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P-PSDB; AAW08147.
P-PSDB; AAW08148.
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misc_difference
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the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. Of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                  51 CAAAAAACCACAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAG 110
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the closely related CHO-1A gene (AAT4275) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-IA give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex determination; chromodomain-Helicase-DNA binding 1 Avian; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The chicken CHD-W gene (AAT42754) acting alone or in conjunction
                                                                                                                                                                                                                                             Score 68.4; DB 18; Length 6608;
Pred. No. 5.7e-10;
); Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                             Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                      111 CAGAGATCTTGCAAAAAGAGAGCTCAGAGACTTTGTGGTGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken CHD-W gene (partial sequence).
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ilarity 79.4%;
Conservative
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                                                                                                                                                                                                                                                               Local Similarity
nes 81; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT42754;
                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bird;
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Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;

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                                                                                                                                                                                                                                                                                                                                                              ds; human; telomere repeat binding factor; A-TRF; dimerisation domain; telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
                                                                               52 AAAAAACCACAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGC 111
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                ó
 Length 1316;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;
                                                                                                                                            112 AGAGATCTTGCAAAAAGAGGCTCAGAGACTTTGTGGTGC 152
   DB 18;
 Score 67.4; DB 18
Pred. No. 7.4e-10;
                                                                                                                                                                                                                                                                                                                                 Altered telomere repeat binding factor 1 gene.
                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Van Steensel B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A-TRF"
                                                                                                                                                                                                                                     AAV59280 standard; cDNA; 1311 BP
44.18; 79.28;
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/product=
                                                                                                                                                                                                                                                                                                    (first entry)
                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-480769/41.
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAW59280
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9836066-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-1998;
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                                80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                Matches
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AAV59280
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2000US-0249215
2000US-0249216
06-SEP-2000; 06-SE
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ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
digestive system disorder; Meckel's diverticulum; ss.
                                                                            Gaps
                                                                                                                                             52 AAAAAACCACAAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTA 105
                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human digestive system antigen coding sequence SEQ ID NO: 1198.
                      Query Match 35.3%; Score 54; DB 19; Length 1311; Best Local Similarity 100.0%; Pred. No. 49e-06; Matches 54; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                           AAK88882 standard; cDNA; 421 BP.
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2000US-0229509
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11-JUL-2000)
14-JUL-2000)
26-JUL-2000)
14-AUG-2000)
13-AUG-2000)
13-AUG-2000)
10-SEP-2000)
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10-SEP-2000)
10-SEP-2000)
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2000US-0216880.
2000US-0217487.
2000US-0217496.
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2000US-0205515
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2000US-0225266
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2000US-0232080.
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                      WO200155350-A1
                                                                                                                                                                         04 - FEB - 2000;
24 - FEB - 2000;
16 - MAR - 2000;
11 - MAR - 2000;
19 - MAY - 2000;
19 - MAY - 2000;
10 - JUN - 2000;
10 - JUN - 2000;
10 - JUL - 2000;
11 - JUL - 2000;
14 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG 2000;

18-AUG 2000;

22-AUG 2000;

22-AUG 2000;

22-AUG 2000;

23-AUG 2000;

30-AUG 2000;

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                                                                                                           17-JAN-2001;
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27-SEP-2000;
                                                                02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendictly, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive system antigen of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 AAAAAACCACAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 aaaaagcctcaggggaagcagctacagacccgagcggattacttgttgaagctgctcaga 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.9%; Score 41.2; DB 22; Length 421; 62.7%; Pred. No. 0.016; 11ve 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 AGAGATCTTGCAAAAAGAGGCTCAGAGACTTTGTGGTGCG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colorectal cancer antigen cDNA SEQ ID NO: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1198; 986pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Barash SC, Ruben SM
                                                                                                                                                                                           20000S-0250160.
20000S-0250391.
20000S-0251030.
20000S-0251988.
20000S-0256719.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI57603 standard; cDNA; 421
                                                                                                                                                                                                                                                                                                                                                     2000US-0251868.
2000US-0251869.
                                                                                                                                                    2000US-0249299
2000US-0249300
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2000US-0251856
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                                                             2000US-0249245
                                                                                                         2000US-0249265
2000US-0249297
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P-PSDB; AAM93109.
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Best Local Similarity
Matches 64; Conserv
                                    17-NOV-2000;
10-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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AAI57603
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The present invention provides the protein and coding sequences of a number of colorectal cancer antiqens. These are shown in AALS7547-AALS75619 and AAMS8569-AAMS8641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen coding sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                          Isolated polypeptide for treating, preventing and/or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection \rm e.g., diagnosts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 AAAAAACCACAAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCAACTACTTAGC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 aaaaagcctcaggggaagcagctacagacccgagcggattacttgttgaagctgctcaga 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic; antiatreriosolerotic; antianemic; cytostatic; nootropic; nootropic; nootropic; noeuropiccetive; anti-HTV; anticonvulsant; ophthalmologic; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antilhifammatcry; cancer; eye disease; arteriosolerosis; anaemia; acute myeloid leukeamia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
26.9%; Score 41.2; DB 22; Length 421;
Best Local Similarity 62.7%; Pred. No. 0.16;
Matches 64; Conservative 0; Mismatches 38; Indels 0;
                                                                                                                                                                  Claim 1; SEQ ID NO: 67; 522pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO: 1004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AGAGATCTTGCAAAAAGAGAGCTCAGAGACTTTGTGGTGCG 153
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 421 BP; 148 A; 78 C; 127 G; 61 T; 7 other;
  Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABE33031/c
ID ABL33031 standard; DNA; 6118 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-2001; 2001WO-EP07537
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Rosen CA, Barash SC,
                                WPI; 2001-457727/49.
P-PSDB; AAM38625.
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Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG.

WPI; 2002-130909/17

(HUMA-) HUMAN GENOME SCI INC.

30-JUN-2000; 2000DE-1032529. 01-SEP-2000; 2000DE-1043826.

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3750 AAAAA 3746
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0
                                                                 The present invention provides a number of human immune system associated depens which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer
                                                                                                                                                                                                                                                                 4191 CGAAAAATATAAAAAAAAAAAATTATCTATATCTAATACTAATACTAATACATATACAAT 4132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                 CAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTTGCAA 124
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                     5 TTCCAGATGATGATAAAAAACCACAAAGCAAAAACAGTTACAGACCAAAAAAACCACAAAG 64
leic acid comprising fragment of chemically modified gene, useful diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour suppressor gene derived chemically modified sequence #106
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                                                                                                                                                                                                          Score 37.4; DB 24; Length 6118;
                                                                                                                                                                       Sequence 6118 BP; 1751 A; 141 C; 1229 G; 2997 T; 0 other;
                                             Claim 1; SEQ ID NO 1004; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                     Pred. No. 0.38
0; Mismatches
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ID AAS46384 standard; DNA; 5649 BP.
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                                                                                                                                                                                                         24.4%;
55.9%;
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2000DE-1019173,
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                                                                                                                                                                                                                               71; Conservative
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                       cytosine methylation
                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             125 AAAGAGA 131
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30-JUN-2000;
  Nucleic acid
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06-APR-2000;
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                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                     11
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                                                                                                                                                                                                                                Matches
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Disagnation of genes associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since oncogenes having a sequence taken from 536 (actually 533 since oncogenes having a sequence taken from 536 (actually 533 since oncogenes having a sequence to from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a form peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may compared of probes for detecting the cytoshme methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for accretaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific compared to another set of genetic and/or epigenetic parameters may be compared to another set of genetic and/or epigenetic parameters which compared to another set of genetic and/or epigenetic parameters. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533 genomic sequences derived from tumour suppressor genes and concogenes. Sequences with even numbered Seq ID numbers are the concogenes. Sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID), ID 536 and ID 535, except for those whose partner sequence is missing).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at from WIPO at the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 AGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGCAGAGTCTTGC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 · 3 TCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGACCAAAAAAACCACA 62
                                                                                           The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; arteriosclerosis; anautinflammatory; cancer; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5649 BP; 1212 A; 184 C; 1397 G; 2856 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.4; DB 22;
Pred. No. 1.4;
0; Mismatches 56;
Claim 1; SEQ ID No 106; 27pp; English.
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Best Local Similarity 55.2%;
Matches 69; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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03-JAN-2002

cytosine methylation

WPI; 2002-130909/17.

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCAACAACTACTTAGCAGAGATCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAAACAGTTACAGACCAAAAAACCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antiatateriosclerotic; antianemic; cytostatic; nootropic; noetropic; enti-HTV; antionvulsant; ophthalmologica; anti-HTV; antionvulsant; ophthalmologica; antiinflammatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anemia; acute myeloid leukeamia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders
                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 5931; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.9%; Score 35; DB 22; Length 413; Best Local Similarity 54.2%; Pred. No. 0.94; Matches 71; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune system associated gene SEQ ID NO: 807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 413 BP; 82 A; 22 C; 74 G; 235 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL32834 standard; DNA; 6283 BP.
                                                                         rang YT, Liu C, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 AAAAAAAAAA 154
                                                                                                                           WPI; 2001-514838/56.
                     (HYSE-) HYSEQ INC.
                                                                                                                                                   P-PSDB; AAO05940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation.
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                                                                                                                                                                                                                                                            disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TCTTCCAGATGATCCTGATAAAAACCACAGAGCAAAACAGTTACAGACCAAAAACCACA 62
                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.1%; Score 35.4; DB 24; Length 5649; Best Local Similarity 55.2%; Pred: No. 1.4; Matches 69; Conservative 7; Mismatches 56; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5649 BP; 1212 A; 184 C; 1397 G; 2856 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 822; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 5931.
                                                                                                                                                                                                                             Olek A, Piepenbrock C, Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI85871 standard; cDNA; 413 BP
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                                           02-JUL-2001; 2001WO-EP07537
                                                                                            30-JUN-2000; 2000DE-1032529
                                                                                                                        01-SEP-2000; 2000DE-1043826
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3750 AAAAA 3746

123 AAAAA 127

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WO200164835-A2.

07-SEP-2001

Homo sapiens.

RESULT 13
AA1858712
XX AA1858716
XX AA18587
XX AA18587
XX AA18587
XX AA18587
XX AA18587
XX Human;
XX Human

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0; Gaps

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 TCCAGATGATCCTGATAAAAAACCACAAAACAGAAAACAGTTACAGACCAAAAAAACCACAAGC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 2393854 AAAATAGTAATAGTCAGCAACAAACAAACAATCACA 2393818
                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                     organisms
                                                                                 Rose M,
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                                                                                                                                                                                                                                           The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reluxemia, Alzheimer's disease, Alzheitepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/vlocrative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 GCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTTGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CTTCCAGATGATCCTGATAAAAAACCACAAAGCAAAACGGTTACAGACCAAAAAACCACAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 24; Length 6283;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H,
                                                                                                                                                                                                                                                                                                                                                                      Sequence 6283 BP; 1407 A; 230 C; 1615 G; 3031 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Indels
                                                                                                                                                                                                                    Claim 1; SEQ ID NO 807; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeria monocytogenes EGD-e genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA03041 standard; DNA; 2944528 BP.
                                                                                                           Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.9%;
Best Local Similarity 55.3%;
           02-JUL-2001; 2001WO-EP07537.
                                      30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Conservative
                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes
                                                                              (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INSP ) INST PASTEUR
                                                                                                                                                                                          cytosine methylation
                                                                                                                                     WPI; 2002-130909/17.
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The present sequence is the genome sequence of Listeria monocytogenes EGD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and to study genetic polymorphisms and other genomes. Proteins (ABB47297-ABB50149) expressed from the present sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. This sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, this sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                          Amend A;
Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez Boland JA; Dominquez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Cakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 1; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-010914/01
                                                                                                                                                                                                                                                                                                                                                        Voss H;
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ö Length 2944528; Indels Score 34.6; DB 24; Pred. No. 11; 0; Mismatches 39; 22.6%; 59.8%; Conservative Query Match Best Local Similarity Matches 58; Conserv

Db 2393914 TTCAAAGTTCCCCTAGCAAATACCCAAAGAATAACAGTTATAAAATCTAATAATTACAATC 2393855 66 AAAACAGTTACAGACCCGTGCAGACTACCTCATCAAA 102

2, 2002, 20:47:17 Search completed: August Job time: 25928 sec

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27.1

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	\sim	 nucleic search, using sw model August 2, 2002, 16:52:08; Search time 8940.62 sea			r of hits satisfying chosen parameters: seq length: 0 seq length: 2000000000	st-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BB155356 BB155356	BB461065 BB461065	BB834922 BB834922		_		BF239967 601905170	AU125712 AU125712	BE895133 601436060	AW997058 QV3-BN004	AW996787 QV3-BN004	AL659353 AL659353	AL644594 AL644594	AL286261 Tetraodon	AL658477 AL658477	AQ275532 RPCI-5-11	AV546625 AV546625
SUMMARIES	ID	BB155356	BB461065	BB834922	BB830730	AL601246	AI890775	BF239967	AU125712	BE895133	AW997058	AW996787	AL659353	AL644594	CNS04DVG	AL658477	AQ275532	AV546625
	99	6	σ	6	6	σ	6	10	ტ	10	σ	6	თ	σ	12	6	12	6
	Query Match Length DB	619	099	446	438	430	547	821	866	1028	989	337	593	645	856	642	352	424
dР	Query	66.7	66.7	62.5	58.4	50.3	50.3	50.3	50.3	50.3	47.2	41.2	37.1	37.1	33.2	27.7	27.5	27.2
	Score	102	102	95.6	89.4	77	77	77	77	77	72.2	63	56.8	56.8	50.8	42.4	42	41.6
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19 41.4 27.1 20 41.2 26.9 22 41.2 26.9 23 41.2 26.9 24 41.2 26.9 25 41.2 26.9 26 41.2 26.9 27 41.2 26.9 28 41.2 26.9 29 41.2 26.9 29 41.2 26.9 20 41.2 26.9 20 41.2 26.9 20 41.2 26.9 20 41.2 26.9 20 41.2 26.9 20 41.2 26.9 21 30 8 8 26.0 31 39 8 26.0 31 39 8 26.0 31 39 8 26.0 31 39 8 26.0 31 39 8 26.0 31 39 8 26.0 31 39 8 26.0 31 39 8 26.0 31 39 8 26.0 31 39 8 26.0 31 39 8 26.0 31 36 8 24.1 41 36 8 24.1 41 36 8 24.1 42 36 8 24.1 43 36 8 24.1 43 36 8 24.1 43 36 8 24.1 44 36 8 24.1 45 36 8 24.1 47 36 8 24.1 48 36.8 24.1 48 36.8 24.1 49 36.8 24.1 41 36.8 24.1 41 36.8 24.1 42 36.8 24.1 43 36.8 24.1 44 36.8 24.1 45 36.8 24.1 46 36.8 24.1 47 36.8 24.1 48 36.8 24.1 49 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 42 36.8 24.1 43 36.8 24.1 44 36.8 24.1 45 36.8 24.1 47 36.8 24.1 47 36.8 24.1 48 36.8 24.1 49 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 42 36.8 24.1 43 36.8 24.1 44 36.8 24.1 45 36.8 24.1 47 36.8 24.1 47 36.8 24.1 48 36.8 24.1 49 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 42 36.8 24.1 43 36.8 24.1 44 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 41 36.8 24.1 42 36.8 24.1 43 36.8 24.1 44 36.8 24.1 41 26.8 41 12.2 42.1 42 36.8 42 11 2.2 42 41 42 36.8 42 11 2.2 42 41 42 41 26.8 42 11 26.8 42									339	619	255						EN full	A clone protein	GI:16268		· ທ	Metazoa; utheria; to 619)	Carninci K., Hori, Matsuv	Okido, T.	Tagawa, A.	ESTS (Ar	2000 this	for Genom	te of Phy	503-9222	me-res@gs	, Shibata H., Okaza	ion and s l-length	me Res ujiwake,S	, Yoneda,
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Notes mouse:

Butaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Butaryota: Metazoa: Chordata; Sciurognathi; Muridae; Murinae; Mus.

Extraction: Carnincip. P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,

Hiramoto, K., Hori, F., Tahii, Y., Ito, M., Kawai, J., Konno, H., Kouda

M., Koya, S., Metsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,

M., Koya, S., Matsuyama, T., Miyazaki, T., Sogabe, Y., Suzuki, H.,

Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,

Muramatsu, M. and Hayashizaki, Y., et al. 2001)

Muramatsu, M. and Hayashizaki, Y., et al. 2001)

AL Unpublished (2001)

AL Soloratory for Genome Exploration Research (RIKEN)

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Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Site_1: Sal1: Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
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/dev_stage="12 days embryo"
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                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.rlken.go.jp/) for
further details.
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/organism="Mus musculus"
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S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
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FEATURES

Query Match

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RESULT BB461065

ACCESSION

BASE COUNT ORIGIN

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"RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
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Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatau,N., Hiranoto,K., Hiraoka,T., Hiraoka,T., Hiraoka,T., Motana,T., Motana,T., Motana,T., Sana,T., Ito,M., Kawah,J., Kojima,Y., Kono,H., Kouda,M., Matauyama,T., Y., Ito,M., Kawah,J., Kojima,Y., Kono,H., Kouda,M., Matauyama,T., Shinata,K., Sakai,K., Sakai,K., Sakai,K., Sasaki,D., Sato,K., Salto,R., Sakai,F., Sakai,K., Sasaki,D., Sato,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Topay,T., Watchiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. et al.
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BBB34952 RIKEN full-length enriched, mammary gland RCB-0527 
Jyg-Wc(R) CDNA Mus musculus CDNA clone G930033421 3', mRNA
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URL.http://genome.gsc.riken.go.jp,

Carnindi,P., Shibatei,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper.selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suelbro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-5222
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wagik., Pujwake,S., Inoue,K., Togawa.Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa.T., Ozawa,K., Tanaka.T., Matsuura
NS., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                           Length 660;
                                                                                                                                                                                                                                                                                                                        66.7%; Score 102; DB 9; Length 660
100.0%; Pred. No. 3.9e-11;
.ive 0; Mismatches 0; Indels
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BBB34922.1 GI:17013165
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(bases 1 to 438)

Akimura T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,

Akimura T., Arakawa, T., Carninci, P., Hirozane, T. Inotani, K., Ishi,

Y. Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,

Nakamura, M., Mishi, K., Nomura, K., Numasaki, R., Okazaki, T., Okido, T.,

Saito, R., Sakai, C., Sakai, K., Sakaume, N., Sasaki, D., Sato, K.,

Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Tamaka, T., Tomaru, A., Toyaru, Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

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URL.http://genome.gsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp,
Carninci.P. Shibata.Y. Hayatsu.N. Sugahara.Y., Shibata.K., Itoh
M., Konno.H., Okazaki.Y., Muramatsu.M. and Hayashizaki.Y.
Normalization and subtraction of cap-trapper-selected coNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagit.K., Pijlwake,S., Inoue.K., Togawa.Y., Izawa.M., Ohara.E.,
Watahiki.M., Yoneda.Y., Ishikawa.T., Ozawa.K., Tanaka.T., Matsura.S.,
Kawai.J., Okazaki.Y., Wuramatsu.M., Inoue.Y., Kira.A. and
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokobama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-72 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Per: 81-45-503-9226
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                               /organism="Mus musculus"
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RCB-0527 Jyg-MC(B) cDNA"
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NCI-OGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 AAAAAACCACAAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:2443725"
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                                                                                                                                                                                                                                                                                                                         Score 77; DB 9; Length 430;
Pred. No. 3.8e-06;
0; Mismatches 5; Indels
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/db_xref="taxon:9606"
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                             RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (11), Rikunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Gerome Analysis, German Cancer
Research Center (DREZ): Email s.wiemannedkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Barunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
Phis clone (DREZp313J1040) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de.
                                                                                                                                                                                                                        encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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RCB-0527 Jyg-MC(B) cDNA"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-WC(B)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AAAAAACCACAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTA-CTTAG 110
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Pred. No. 1.3e-08;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL601246.1 GI:15164752
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                             e mouse tissues.
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DEFINITION

RESULT AL601246

ACCESSION

VERSION

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

KEYWORDS SOURCE

Query Match

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BASE COUNT ORIGIN

FEATURES

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Fax: 81-438-52-3952
                                                                                                                                                                                                                                    Homo sapiens
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Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                     sequence.
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                                                                                            DEFINITION
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                           RESULT
AU125712
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/tab_nost="bHi0B" (TI phage-resistant)"
/note="Organ bone marrow; Vector: pDNR-LIB (Clontech);
/note="Organ bone marrow; Vector: pDNR-LIB (Clontech);
/note="Isfal (ggcgcctcggcc); Site_2: Sfil (ggccattatgcc);
/nouble-stranded CDNN was prepared from cell line RNA.
/s' and 3' adaptors were used in cloning as follows: 5'
/adaptors sequence: 5'-CACGCCATTAGGCC3' and 3' adaptor
/sequence: 5'-ATTCTAGAGCCGAGCGCGCACATG-dT(30)BN-3'
/where B = A, C, or G and N = A, C, G, or T).
/note inserts size_1.75 k (range o.9-4, 0 kb). IS/15 colonies
/note inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech
/aboratories (Palo All 7).
/adaptories (Palo All 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliai Eutenta; Primates; Catarrhini; Hominidae; Homo.

En (bases 1 to 81)

NIH-WGC http://mgc.nci.nih.gov/.

NIH-WGC http://mgc.nci.nih.gov/.

Ontact: Robert Strausberg, Ph.D.

Email: Gapba: refmail.nih.gov

Tissue procurement: ATC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Prayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIAN at:

http://image.llni.gov

Plate: LiCkNlO3 row: k column: 18

High quality sequence stop: 562.
                                                                                                                                                                                                                                                                                                     BF239967 821 bp mRNA linear EST 14-NOV-2000 601905170F1 NIH_MGC_54 Homo saplens cDNA clone IMAGE:4133129 5',
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                                           52 AAAAAACCACAAAACAATTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGC 111
                                                                    357 AAAAAACCACAAACAGTTGCAGACCCGTGCAGACTACCTCCATCAAATTACTTAGT 298
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  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.3%; Score 77; DB 10; Length 821; 94.1%; Pred. No. 3.3e-06; tive 0; Mismatches 5; Indels
     5; Indels
0; Mismatches
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_54"
                                                                                                                                        112 AGAGATCTTGCAAAAAGAGGGCTC 136
                                                                                                                                                           297 AGAGATCTTGCAAAAAAAGAAGCTC 273
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                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BF239967
BF239967.1 GI:11153890
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  Conservative
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80;
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TITLE
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KEYWORDS
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1028 bp mRNA linear EST 20-OCT-2000 601436060F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3921087 5', BE895133
AU125712 866 bp mRNA linear EST 23-OCT-2000 AU125712 NT2RM4 Homo sapiens cDNA clone NT2RM4002061 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
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                                                                                                                                                                                                                                                                                                                                                                                               HEI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saico,K., Yamamatco,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
153-3 Yana, Kisarau, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1028)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 86)

Ota,T., Wakamateu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genomics@hri.co.jp
Hrl human cDNA project; 5' & 3'-end one pass sequencing: Helix
Hrsearch Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4002061"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 AGAGATCTTGCAAAAGAGAGGCTC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor cells"
149 c 196
                                                                                      AU125712
AU125712.1 GI:10950428
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337 bp mRNA linear EST 05-JUN-2000 QV3-BN0047-230200-102-d03 BN0047 Homo sapiens cDNA, mRNA sequence. AW996787. GI:8257021
                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
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/dcolore_lib="BN0047"
/dcolore_lib="BN0047"
/dcolored_lib="BN0047"
/note="Organ: Preast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpsonelouding.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-230 200-102-d03&t3=2000-02-23&t4=1) Seq primer: puc 18 forward High quality sequence start: 2 High quality sequence stop: 337.
Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2=0V3-BN0047-150 400-152-c08513-2000-04-15&t4=1) Seq primer: puc 18 forward High quality sequence start: 19 High quality sequence stop: 678. Location/Qualifiers
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 686;
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llarity 96.1%; Pred. No. 3.1e-05;
Conservative 0; Mismatches 3;
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154 c 126 g 241 t
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                           T. .686
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                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
cLone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
//do.arificra.llnl.gov
//do.arificra.lln
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 686)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Magai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
Simpson, A.J.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
National Institutes of Health, Mammallan Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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20202663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.3%; Score 77; DB 10; Length 10 larity 94.1%; Pred. No. 3.2e-06; Conservative 0; Mismatches 5; Indels
                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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205 c
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/ ..645
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/db_zref="taxon:8364"
/clone_lib="xGC-egg"
/dev_stage="egg"
/de
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                  52 AAAAAACCACAAAAGCAAAAACAGTTACAGACCGGTGCAGACTACCTCAAACTACTTAGC 111
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Bmall: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: Libidi2.plc
Sequencing primer: PlC
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
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11 Similarity 73.0%; Pred. No. 0.035;77 Indels (73; Conservative 0; Mismatches 27; Indels (
Best Local Similarity 73.0%; Pred. No. 0.035;
Matches 73; Conservative 0; Mismatches 27; Indels
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AL644594.1 GI:16796719
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1 (bases 1 to 645)
Huckle, E., Taylor, R., A
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                                                                                                                                                                                        /note="organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under 10w stringency conditions.
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/dev_stage="neurula"
/lab_host="Escherichia coli DH10B".
/note="Vector: pc5107; Site_1: EcoRI; Site_2: NotI; CDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pc5107 with
EcoRI at the 5' end and NotI at the 3' end."
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Slutrana tropolcalis
Eukaryotes, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
Xenopodinae; Slutrana.
I (bases 1 to 593)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sangar Xenopus tropicalis EST project 2001 (10_2001)
Contact: Huckle
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Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xanopus tropicalls EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu045e20.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63; DB 9; Length 337;
Pred. No. 0.0024;
0; Mismatches 5; Indels

    .593
    /organism="Silurana tropicalis"
/db_xref="taxon:8364"

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/clone_lib="XGC-neurula"
                                                                 /organism="Homo sapiens"
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/dev_stage="Adult"
Location/Qualifiers
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Matches 78; Conservative
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Sanger Centre
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Job time: 12213 sec
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                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia: Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae: Silurana.
1 (bases 1 to 642)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Contact: Huckle E
                                                                                                                                                         Tetraodontidae; Tetraodon.

Tetraodontidae; Tetraodon.

Tobases 1 to 856)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                  Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 856)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a lar
scale clone-end sequencing project of the Tetracodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="103K08"
/clone_lib="6"
/note="Genoscope sequence ID : COBG103BF04LP1-end : T7"
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              AL286261.1 GI:8024707
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_ESQUENCE_ID: TNeu045p04.sp6
Sequencing primer: SF6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
1. .642
//organism="silurana tropicalis"
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/clone="inaud45p04"
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/lab_host="Escherichia coli DH108"
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Pred. No. 25;
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August 2, 2002, 20:29:35 ; Search time 12674 Seconds (without alignments) 252.625 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                       US-08-973-363-3
153
1 ATTITACCTGATGATCCAGA......CACAAAGGCTTGCTGGTGCA 153
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Description

SUMMARIES

Result Query
No. Score Match Length DB

A58684 Sequence 4 A58685 Sequence 4 A58685 Sequence 5 A58661 Sequence 15 A58691 Sequence 12 A58691 Sequence 2 A58696 Sequence 2 A58696 Sequence 12 A58691 Sequence 12 A58651 Sequence 12 A58651 Sequence 2 A58661 Sequence 3 A56661 Sequence 3 A56661 Sequence 3 A56661 Sequence 3 A56661	AC001449 Homo sap AC006331 Homo sap AC006331 Homo sap AC01246 Homo sap AC022181 Homo sap AC022182 Homo sap AC022182 Homo sap AC02282 Homo sap AC02763 Sequence AX33315 Sequence AX3315 Sequence AX3315 Sequence AX3315 Sequence AX017483 Homo sap AC01700 Homo sap AC022018 Wus muscu AC02218 Wus muscu AC02218 Wus muscu AC02218 Wus muscu AC02218 Homo sap AC012006 Homo sap AC012006 Homo sap AC012006 Homo sap AC012006 Homo sap AC021302 Homo sapien AR02381 Human DNA AC012102 Homo sapien AC01702 Homo sapien AC010702 Homo sapien AC01070 Homo sap	PDNA Linear PAT 06-MAR-1990 05. IN METHODS FOR SEX IDENTIFICATION IN 1996; ed" 24 t
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153 140.2 130.6 103 103 102.4 77.8 67.4 62.6 62.6	E400789001924400200019244000001102400000000000	H Z Z Z H
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Length 153;

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unclassified.
I (bases 1 to 6608)
Griffiths.R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS
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2.1e-20;
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Pred. No. 1.1e-28;
0; Mismatches 14
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
1. .6608
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100.0%; Pred. No. 2.1
ive 0; Mismatches
                                       Patent: WO 9639505-A 5 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224
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/db_xref="taxon:32644"
1207 c 1459 g 1653
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/db_xref="taxon:32644"
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Pred. No. 1.5e-31;
0; Mismatches 8;
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                                         Score 153; DB 6;
Pred. No. 2.2e-35;
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ISIS INNOVATION (GB)
Other publication AU 596696 961224
Location/Qualifiers
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A58686
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Sequence 4 from Patent WO9639505.
A58685
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Griffiths, R. and Tiwari, B.
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                                      Query Match 100.
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Matches 145; Conserv
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Length 6872;

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Query Match 67.3%; Score 103; DB 5; L
Best Local Similarity 100.0%; Pred. No. 2.1e-20;
Matches 103; Conservative 0; Mismatches 0;
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STGRRGATATTIAVERABETKTDSDDLLEUGEBUNGGARNGWARNGANGHANG
STGRRGATTIAVERABLEDDBAGGERKSKELGETGYLLKRGWSHIHWWEDEBT
SKGRWATGASTTIAVERDDBAGGARAR KREGARIDEDBLHKGWGINETTIETTE
KKQUNYGMRKLDHYKKRODGETKSRWERNASPEDGALLKRYGARIDEDBLHKGWGINETTIETTE
CKYLKORPREYALKKOPGETYSERGAGALLKRYGARIDEDBLHKGWGINETTIETTE
KTIOTISFLNYLFHEHQLYGPTLRVPLSTLTSWQREIGTWAPQWANVYLGDITSRN
MITHTERMHOLTIGTTYSELLKASPELGGANRAFTOYDBAHRKRNDSLLY
KTIOTISFLNYKRODRSLAANVOLLKASPELGHNAFTOYDBAHRKRNDSLLY
KTIOTISFLARWKKOPKSLAANVOLLKASPENGETANYGORALOHITRANYKAS
STSGFLNIMMELKKOVEKSLAANVOLLKROPROLOSIKGELRKQALDHFNAEGSEDFG
FLLSTRAGGINIAASADYYTDSDAWNONDONLOGRONNYKES
VEEDILERRAKKKWYLDTLAZYLKYRQFFORLOGSIKGELRKQALDHFNAEGSEDFG
FLLSTRAGGINIAASADYYTOKTVLHGGSTSESTPRYKEELSALLKFGAREE
LEPERABSRWWELIFSGORFREEERROFFYTOGELLGSTRYNDEDDIE
LEPERABSRWWELIFSGORFREEERROFFYTOGELLGSTRYNDEDDIE
LEPERABSRWWELITSGORFREEERROFFYTOGELGSTRYNDEDDIE
                                                                                                                           RUATYOCAS Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 6072)

Griffiths, R. and Korn, R.M.

A CHDI gene 1s Z chromosome linked in the chicken Gallus domesticus Gene 197 (1-2), 225-229 (1997)
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ESEEDHOKTFSVCKERRRPVKAALGALDRPSKEGLSREDGLEHTRGCLIKIOHITECL
KETYNPEOLYGORKULAIFVSKFTEFDARLJKLYKHAIKKOEGENGHUNDONISSNVN
THVIRENDVERKETYNHDDSSRDSYSSDRHLSOYHDHHKDHHGCDAYKSGDSRRRPY
SAFSNGKDHHRNDTHKGDSRYXGDSRNSYSDRHSKDHSCHSCHSPRIGGNLKOSPGGREDHRSH
SDHRIHSDHRSTSEYSHHKSDROYRTHSDWONDHRASGSGPRSPLDGRSPGGREDHSH
HSCPPENSSDHKSTPSEYSHHKSRDYRTHSDWONDHRASGSGPRSPLDGRSPGGRSPLG
A131. 4604
//gene="CHD-2"
//gene="CHD-2"
//fore="CHD-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University,
Glasgow G12 8QQ, UK
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LKKOQOQORAASSDSGSEDSSSSEDSADDSSSETKKKKINKDEDWOWSGSGSVSGTGS
DSESABOGUSSSCESSESDYEPKNVKSRKPPSRIFKRSGKKSTGOKKRQLOSSEBER
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OVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHPDIDMGKEDDSNLLVGI
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RLAGGAGSRRRYTRKTKKMKAKTSKIEDIKOSPOPJSRAGSBODDEEDIKDBIYSYK
HLHKYIKTWEKRERPERPOJGJIKKEAERERRETKEERIKREKKREKEDKREKKEKEKKEKEK
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/gone="CBD-2"
/fonction="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gallus gallus"
/db_xref="taxon:9031"
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Griffiths,R. and Korn,R.M.
Direct Submission
Submitted (16-MAY-1997)
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AF004397.1 GI:2501845
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AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                  4100 CAAGAAACCCCAGGCAAAGCAGCTACAGACCGTGCAGACTACCTCATTAAATTACTGAA 4159
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
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Sequence 15 from Patent WO9639505.
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Sequence 2 from Patent W09639505.
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A58683.1 GI:3714246
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/db_xref="taxon:32644"
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Submitted (29-JAM-1993) Jun-ichi Funahashi, Inst. Devel., Aging and
Cancer. Toboku Univ.; 4-1 Seiryo-machi, Aoba-ku, Sendai 980-77,
Japan (Tel:022-272-9499, Fax:022-272-3982)
                                                                                                                                                                                                                                                                                                                                                                                                            VRT 03-FEB-1999
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FGAEELFKEPEGEEQEPQEMDIDEILKRAETRENEFGPLTVGDELLSQFKVANFSNMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDDIELEPERNSRNWEETIPESQRRRIEEEERQKELEEIYMLPRMRNCAKQISFNGSE
GRRSRSRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGP
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RISGVQVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDWGKEDDSN
LLVGIYEYAYGSWQCKVNGSRSQLNTEILPDDPDRTPRQNSYRPVQTTSLNY"
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SEDFCFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRL
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//note="beta-gal fusion protein binds to blocks 10 to 3 of
HN fragment of delta-crystallin enhancer."
/codon_start-i
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                             1159 AAGAAACCCCAGGCTAAGCAGTTACAGACTCGTGCAGATTACCTCATTAAATTACTGAAT 1218
                                                                                                                                                                                                       52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAAT 111
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Funahashi,J., Sekido,R., Murai,K., Kamachi,Y. and Kondoh,H. Delta-crystallin enhancer binding protein delta EF1 is a zinc finger-homeodomain protein implicated in postgastrulation
                                                                                                                                                                                                                                                                                                                                                                                              014316 delta crystallin enhancer binding protein, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (library: lambda gt11) 13 day embryo lens cDNA
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                                                                                                                                  Length 1316;
                                                            others
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                                                                                                                                                                                                                                                                                                112 AAAGACCTTGCAAGAAAGGAAGCACAAAGGCTTGCTGGTGCA 153
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Pred. No. 3e-17;
                                                                                                                                  Score 92.4; DB 6;
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                                                                                                                                                                      0; Mismatches
                                                          304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             embryogenesis
Development 119 (2), 433-446 (1993)
1. .1316
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a 205 c 308 g 30
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                                                                                                                                60.48;
94.18;
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Funahashi,J.
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                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA, clone JF11.
Gallus gallus
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AUTHORS
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JOURNAL
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TITLE
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JOURNAL
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SOURCE
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SQSGSSDSDSGSGSGSESEDT ARRONGAR PPKYDGAEFWKSSPSTLAVQRRAML
RKQPQQAQQQRPASSNSGSEDSSSSEDSDSSSGAKKKHNDEDWQMSGSGSPSGLG
SDSSESEERRKSSCOTTESDYEPKWKVRSKREQMRSKSKNGKKLTGQKKRQIDSSEDE
SDSSESEERRKSSRQATWWSYKEDBEMKTDSDDLLEVCGOKRQIDSSEDE
DDEDYDUNGKSSRRQATWYSYKEDBEMKTDSDDLLEVCGORPQPEDEFFFT ERWW
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SCHEEPFLRRYKKDVBKSLPARVEGGILAMEMSALQKQYYKWILTRRYKALSKGSK
GSTSGFLNIMMELKKCCNHCYLIRPPDNNEFYNKQBALQHLTRRYKALSKGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 5149)
Delmas, V., Stokes, D.G. and Perry, R.P. A mammalian DNA-binding protein that contains a chromodomain and an SNE2/SWIZ-like helicase domain
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ELEPERNSKNWEEIIPEEQRRRLEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRS
RSRRYSGSDSDSISERKRPKKRGRPPTIPRENIKGFSDAEIRRFIKSYKKFGGPLERL
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CFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGOKKOVNIYRLVTKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA On Feb 16, 1994 this sequence version replaced gi:293322.
                                                                                                                                                                                                                                                                               53 AGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAATA 112
                                                                                                                                                                                    Gaps
                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993) 93211972
                                                                                                                        Length 2292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse DNA-binding protein (CHD-1) mRNA, complete cds. L10410 X66028 L10410.1 GI:455014
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                    1943 AAGACCTTGCAAGAAAGGAAGTCGCTAAAGGCTTGCTGGTGCA 1985
                                                                                                                                                                                                                                                                                                                                                                 113 AAGACCTTGCAAGAAAGGAAG--CACAAAGGCTTGCTGGTGCA 153
                                                                                                                    Score 77.8; DB 5;
Pred. No. 7.1e-13;
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                                                                                                                                                                                0; Mismatches
534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="plasmacytoma"
1. .5349
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546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="CHD-1"
                                                                                                                    50.8%;
91.3%;
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Perry, R.P.
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DNA binding protein.
O
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382
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                                                                                                                                                    Similarity
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BASE COUNT ORIGIN AC092372/c RESULT 11 KEYWORDS VERSION TITLE COMMENT g Submitted (03-JUN-1997) Laboratory of Gene Transfer, National Human Genome Research Institutes, National Institutes of Health, 49 Convent Drive, Bethesda, MD 20892-4442, USA ö mRNA linear PRI 27-NOV-1997 FMDCRIGRKGATGATTĪTYAVEADGDPNAGFEKNKEPGEIQYLIKWKGWSHIHNTWET
EETIKQQNYRGMKKLDNYKKKDGETKRMIKNASPEDVEYTVCQGEIJDDLHKQYQYG
RIIANGOKARAGYPDYCKWGGLPYECSWEDGALISKKPGACIDEYFSNQSKTTP
FROCKVIKQRPRFYALKKOPSYIGGHEGLEKBYQINGINMIAHSWCKGNSCILLADEM
GLGKTIQTISFLAYLFHEHQLYGPFLLVVPLSTLTSWQNEIQTWASQMNAVVILGDIN DAIARDAELVDKSETDLRRLGELVHNGCVKALKDSSSGTERAGGRLGKVKGPTFRISG VQNNAKLVIAHEDELIPLHKSIPSDPEERKQYTIPCHTKAAHFDIDWGKEDDSNLLIG Eukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 5947).

Woodage_T., Basrai,M.A., Baxevanis,A.D., Hieter,P. and Collins,F.S. Characterization of the CHD family of proteins

Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997) KKQQOQQQQHQASSNGGSEEDSSSSEDDSSSEVRRKHKDEMQMGGGGGPBQS GSDSESEERRKSGCDTESDYPRNKVKSRKPQNRSKSKNGKKLLGGKRQ1DSSBE GDDEEDYDUNGSSRRQAIVNVSYKEDBEMKTDSDDLLEVGEBYPQPPEEEETIER 52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAAT 111 0; Gaps 44.1%; Score 67.4; DB 10; Length 5349; ilarity 79.2%; Pred. No. 9.3e-10; Conservative 0; Mismatches 21; Indels 0; 4107 AGAGATCTTGCAAAAAGAGGCTCAGAGACTTTGTGGTGC 4147 112 AAAGACCTTGCAAGAAAGGAAGCACAAAGGCTTGCTGGTGC 152 Homo sapiens CHD1 mRNA, complete cds. AF006513 /map="5q15-21; near WI-5811" 1. .5947 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="5" /protein_1d-"AAB87381.1" 'CHD1" /codon_start=1 AF006513.1 GI:2645428 /gene="CHD1" 164, .5293 /gene="CHD1" 2 (bases 1 to 5947) Woodage,T. /product-" Direct Submission Local Similarity les 80; Conserva Homo sapiens 1739 a Query Match BASE COUNT ORIGIN Best Loca Matches DEFINITION RESULT 10 ORGANISM ACCESSION AUTHORS gene REFERENCE JOURNAL REFERENCE AF006513 KEYWORDS CDS FEATURES

SRNMIRTHEWTHHOTKRIKFNILLITYEILLKÖKAPLGGLNWAFIGVDEAHRLKNDDS
LIKYKTLIDFRSGNHRLLITGFPLONSLEGHWAFIGGLNWAFIGVDEAHRLKNDDS
TALKYKLIDFRSGNHRLLITGFPLONSLEGHWERTSALLGROTTENERSALDFEERERGKGRREG
SASCHTSGETANTWEREKKCCHHOTLIREDALUSALUS ANGENLOHLERSGKTILLDKLI
RKRETSGNRVIIFSGNWYRLDILAETLKYROPPEPRILCSGIKGELRKOALDHINAEGSE
DPCFLLETRAGGLGIHLAADDTVYIFDSDWNDONDLOAQARAHIGGKKOWNIYRLVT
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ABELFREDEGEODEDOEDDILTURANTGKTVLHTGGASPEPRIEELSAILKFG
ABELFREDEGEODEDOEDDILTURANTGKTVLHTGGASPEPRIEELSAILKFG
ABELFREDEGEODEDOEDDILTURANTGKTVLHTGGASPERRICKOKKOPNIYRLVT
GASVEDDILAETRAKKKWALDHIVORDHOTGKTVLHTGGASPERRICKOKKOPNIYRLVT
ABELFREDEGEODEDOEDDILTURARDTGKTVLHTGGASPERRICKOKKOPNIYRLVT
GASVEDDILATASKNAWEIIVENGCIKARARTRYRKTGASPERRICKOKKOPNIYRL
ISCHVANTALSHEEBLIPHKSIPODEBRICKOTT TCHTKAARTDIOMGREDDONLL
IGITYECYGSWENIKANDFOLSITHKILDDDDNKRQAKQHQARQLQTRADYILKLLSRDLAKK
ALSAGAGSRRRAARAKKRAMKSIKVEREIKSDSPLDSBROKLGSEKSÖGR
ERSKRSSYRRAARAKKRAMKSIKVEEIKSDSPLDSBROKLGSEKSÖGR
ERSKRSSYDRAPHTTAGGEPVPISESEELDOWTFSICKERMRPVKAALKQLDRPEK
GLSERROLEHTRQCLIKIGDHITTECLKEYTPPDQIKQDRYRTSGONSDDDNLESSKSORHLING
YHDHRORHQGOSTRKRSDSKRRPSSEELDOWTFSICKERNRPWRAALKONDH
RASSSGORRSDLONGSNLAPHYNRDPVERRIKKENTHNESRDYRYTBODH
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RASSSGORRSPLDORSSTGSRSPFRIKBLIDDH
RASSSGORRSPLORGSRENDYRHKSTPEHTWSSKTT"

2130 a

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0; Gaps Ouery Match 41.0%; Score 62.8; DB 9; Length 5947; Best Local Similarity 77.6%; Pred. No. 2.2e-08; Matches 76; Conservative 0; Mismatches 22; Indels 0;

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PRI 07-DEC-2001 AC092372 101220 bp DNA linear PRI 07-DEC Homo sapiens chromosome 5 clone RP11-58M12, complete sequence. AC092372 AC092372.3 GI:17402768 DEFINITION ACCESSION

Unpublished

(bases 1 to 101220)

(bases 1 to 101220)

Direct Submission

Submitted (03-UUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

DOE Joint Genome Institute and Stanford Human Genome Center. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101220)

DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission Homo sapiens ORGANISM REFERENCE AUTHORS TITLE REFERENCE AUTHORS

Direct Submission

L. Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA

Draft Sequence Produced by DOE Joint Genome Institute

Waw.j91.doe.gov

Waw.j91.doe.go TITLE JOURNAL JOURNAL REFERENCE

FEATURES

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Submitted (31-007-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (01-UNN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
( Cases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.
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DD 118268 AAAAAACCACAAGCAAAACAGTTGCAGACCCGTGCAGACTACCTCCATCAATACTTAGT 118327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 13436)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                    ACU12624 134365 bp DNA linear PRI 21-JUL-
Homo sapiens chromosome 5 clone CTD-2082I17, complete sequence.
AC012624
                                                                                                                                                                                                                                52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAAT 111
                                                                                                                                                                                               Gaps
                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62.6; DB 9; Length 134365;
Pred. No. 2.7e-08;
0; Mismatches 14; Indels 0;
                                                                                                                                                        Length 101220;
                                                                                                                                                                                               14; Indels
                                                                                                                                                        Score 62.6; DB 9;
Pred. No. 2.7e-08;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'clone="CTD-2082117"
24497 c 25503 g 43951
                                                                    /clone="RP11-58M12"
18862 c 17827 g 30409
1. .101220
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                    112 AAAGACCTTGCAAGAAAGGAAGCAC 136
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DOE Joint Genome Institute.
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                                                                                                                                                          Query Match
Best Local Similarity 83.5%;
                                                                                                                                                                                             71; Conservative
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Unpublished
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Best Local
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TITLE
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REFERENCE
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SOURCE
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All Dipublished

Streen, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barran, N., Beder, F.,

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Bayuslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

DeArellano, K., Dewar, K., Domino, M., Doyle, M., Erenstor, J.,

Ferreira, P., FitzHugh, M., Forrest, C., Gage, D., Galagan, J.,

Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,

Macdonald, P., Marquis, M., Meswan, P., McGurk, A., McKernan, K.,

McMenters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,

Norman, C.H., O'Connor, T., O'Donnell, P., O'lovar, T. M., Peterson, K.,

Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,

Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,

Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,

Direct Submission

Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                        AC021449 143079 bp DNA linear HTG 10-SEP-2000
Homo sapiens clone RP11-58M12, WORKING DRAFT SEQUENCE, 10 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143079)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo, sapiens, clone RP11-58M12
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * arbitrary. Gaps between the contigs are represented as *runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently * consists of 10 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 4.6 in Q20 bases; agarose-fp Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: 15154

Center clone name: 58 M 12

Center clone name: 58 M 12

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Assembly program: Phrap, version 0.960731

Consensus quality: 134743 bases at least Q40

Consensus quality: 139227 bases at least Q30

Consensus quality: 14000; agarose-fp

Insert size: 144000; agarose-fp

Insert size: 142179; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of reads
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Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Db 118328 AGAGATCTTGCAAAAAAAGAAGCTC 118352
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                        AC021449
AC021449.3 GI:10047806
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38820: contig of 38820 bp in length

AAAGACCTTGCAAGAAAGGAAGCAC 136

112

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Consensus quality: 139128 bases at least Q40
Consensus quality: 142756 bases at least Q30
Consensus quality: 14274 bases at least Q30
Consensus quality: 143744 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
Quality coverage: 6.7 in Q20 bases; pulse field gel estimation
(unsity coverage: 6.7 in Q20 bases; pulse field gel estimation

**NOTE: This is a 'working draft' sequence. It currently

**consists of 7 contigs, Gaps between the contigs

**are represented as runs of N. The order of the pieces

**is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

**provided by the submittor.

**This sequence will be repeaced

**by the finished sequence as soon as it is available and

**the accession number will be preserved.

** 56775 56743 gap of unknown length

** 56775 100974: contig of 56774 bp in length

**113128 113127: contig of 44600 bp in length

** 113128 113127: contig of 44600 bp in length

** 113128 113127: contig of 44600 bp in length

** 113128 113127: contig of 44600 bp in length

** 113128 113127: contig of 44600 bp in length

** 113128 1131327: contig of 44600 bp in length

** 113128 113127: contig of 44600 bp in length

** 113128 113127: contig of 1404 bp in length

** 113128 113127: contig of 1404 bp in length

** 113128 113127: contig of 1404 bp in length

** 113128 113127: contig of 1404 bp in length
                                                                                                                                                                                                                                                                         Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 14, 2001 this sequence version replaced gi:7528342.
------Genome Center
Center: Joint Genome Institute
Center Code: JGI
                            Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 145659)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5

Unpublished
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/clone="CTC-480B11"
/clone="CalTech human BAC library C"
42561 a 26309 c 27580 g 48609 t 600 others
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123397: app of unknown length

18 14569: contig of 22262 bp in length.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
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/db_xref="taxon:9606"
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DOE Joint Genome Institute.
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Best Local Similarity 83.55
Matches 71; Conservative
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ORIGIN
                            ORGANISM
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AUTHORS
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JOURNAL
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                                            44412 40511: gap of 400 bp 44512 43791: gap of 45012 43791: contig of 2768 bp in length 44280 47399: gap of 100 bp 45180 46905: contig of 3526 bp in length 47006 51830: contig of 3526 bp in length 47006 51830: contig of 4882 bp in length 51831: gap of 100 bp 51831 51931: gap of 100 bp 6262 6279: gap of 100 bp 6262 6279: gap of 100 bp 6262 75409: contig of 10689 bp in length 5569: gap of 100 bp 75509 92516: gap of 100 bp 100 bp 100409: contig of 13793 bp in length 106410 105509; gap of 100 bp 100 bp 100510 143079: contig of 35570 bp in length 106510 143079: contig of 35570 bp in length 106510 10509: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       906 others
88821 38920: gap of 100 bp
8821 40411: contig of 1491 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP11-58M12"
/clone="RP11-58M12"
1.08820
/note="ssemily_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector_side:right"
43971 a 26246 c 26678 g 45278 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment" 43380. 46905
/note="assembly_fragment" 47006. 51830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51931. .62619 //note="assembly_fragment" 62720. .75408 //note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12617, 106409 // inote="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106510. .143079
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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38921. ,40411
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AC008531
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VERSION
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JOURNAL REFERENCE

ACCESSION VERSION KEYWORDS

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1 Similarity 83.5%; Pred. No. 2.7e-08;
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Consensus quality: 180259 bases at least Q30
Consensus quality: 180259 bases at least Q30
Consensus quality: 184175 bases at least Q30
Consensus quality: 184175 bases at least Q30
Consensus quality: 184175 bases at least Q30
Estimated insert size: 204599; agarose-fp estimation
Batimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation
* NOTE: This is a "working draft' sequence. It currently
* consists of 33 contigs. The true order of the pleces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                            AC091946 193446 bp DNA linear HTG 09-JUN-2001
Homo sapiens chromosome 5 clone RP11-36012, *** SEQUENCING IN
PROGRESS ***, 33 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193446)
DOE Joint Genome Institute.
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s: gap of unknown length
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s: gap of unknown length
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r: contig of 1974 bp in length
r: contig of 1474 bp in length
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4. \SIDS1/gcgdata/hold-geneseq/geneseqn-embl./Na1981.DAT: *
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5. \SIDS1/gcgdata/hold-geneseq/geneseqn-embl./Na2001.DAT: *
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5. \SIDS1/gcgdata/hold-geneseq/geneseqn-embl./Na2001.DAT: *
5. \SIDS1/gcgdata/hold-geneseq/geneseqn-embl.
                                                                                August 2, 2002, 20:47:17; Search time 1205.34 Seconds (without alignments) 217.937 Million cell updates/sec
                                                                                                                                                           1 ATTITACCIGATGATCCAGA......CACAAAGGCTIGCTGGTGCA 153
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                       1736436 seqs, 858457221 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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153
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Human immune system water optimized VI Maize optimi

Prohibitin gene in Human prohibitin g Drosophila melanog immune/haema

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Chick CHD-1A gene	Chick CHD-W gene f	Great tit CHD-W ge	Chicken CHD-1A gen	Mouse CHD-1 gene (Chicken CHD ⋅W gene	Altered telomere r	Human digestive sv	Human colorectal c
SUMMARIES			ΩI		AAT42757	AAT42758	AAT42759	AAT42751	AAT42756	AAT42754	AAV59280	AAK88882	AA157603
			98	1 1	8	18	18	18	78	18	13	22	22
			Score Match Length DB I		153	153	153	6608	153	1316	1311	421	421
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			Score		153	140.2	132.2	103	102.4	92.4	42.8	38.2	38.2
		Result	No.	,	-	7	m	4	5	9	7	8	o

(ISIS-) ISIS INNOVATION LID

/*tag= a /note= "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3" Bird; sex determination; chromodomain-Helicase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss. Key Location/Qualifiers misc_difference 52..81 96WO-GB01341 95GB-0011439 Chick CHD-1A gene fragment. 12-MAR-1997 (first entry) WO9639505-A1. 06-JUN-1995; 05-JUN-1996; 12-DEC-1996. Gallus sp. in

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61 caggctaagcagttacagacccgtgcagattacctcattaaattactgaataaagacctt 120
                                                                                                                                         Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT47758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42715) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAATAAGACCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATTITACCTGATGATCCAGACAAGAAACCCCAGGCAAAGCAGCTACAGACCAAGAAACCC
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                                                    Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                             Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                91.6%; Score 140.2; DB 16
94.8%; Pred. No. 1.3e-33;
ive 0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GCAAGAAAGGAAGCACAAAGGCTTGCTGGTGCA 153
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52..81
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                                                                                                           Claim 8; Fig 3; 76pp; English.
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Best Local Similarity 94.8'
Matches 145; Conservative
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WPI; 1997-043127/04.
P-PSDB; AAW08148.
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P-PSDB; AAW08149.
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                                                                                                                                                                         Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology chicken CHD-1A (A = Avian) gene (AAT47757), chicken CHD-M (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATTITACCTGATGATCCAGACAAGAAACCCCAGGCAAAGCAGCTACAGACCAAGAAACCC
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                                                                                      Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                               Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 gcaagaaaggaagcacaaaggcttgctggtgca 153
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52..81
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                                                                                                                                             Claim 8; Fig 3; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100. Matches 153; Conservative
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/note= '
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Tiwari B;
                                 WPI; 1997-043127/04.
                                                  P-PSDB; AAW08147
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misc_difference
Griffiths R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAATAAAGACCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATTITACCTGATGATCCAGACAAGAAACCCCAGGCAAAGCAGCTACAGACCAAGAAACCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 attttacctgatgatccagataagaaaccacaggcaaagcagttgcagaccaagaaacca 60
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                   Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                                                                                                             DB 18; Length 153;
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86.4%; Score 132.2; DB 18; Length
Best Local Similarity 91.5%; Pred. No. 3.6e-31;
Matches 140; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                       Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
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228..5390
/*tag= a
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                                                                                        Claim 8; Fig 3; 76pp; English
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4100 caagaaaccccaggcaaagcagctacagacccgtgcagactacctcattaaattactgaa 4159
The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-IA gene (AAT47751) is suggested to initiate female development in birds. The sequence of CDH-IA was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA ibrary using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-IA (A - Avian) gene shows close identity to the mouse CHD-I gene (see also AAT42756-57). It is located on an autosome or 2 chromosome. Probes based on CHD-W and CHD-IA give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. Of a bird. CHD-IA qive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 CAAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                             acids can also be used to control the sex of the progeny of a bird.
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bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.3%; Score 103; DB 18; Length 6608; Best Local Similarity 100.0%; Pred. No. 9.9e-22; Matches 103; Conservative 0; Mismatches 0; Indels 0;
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birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse CHD-1 gene (bases 3855-977).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_difference 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW08146
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Length 1316;

Similarity

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           Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, focus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                  61 CAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAATAAAGACCTT 120
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                 9
see also AAT42758) and the great tit CHD-W gene (see also AAT42759)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex determination; chromodomain-Helicase-DNA binding 1 Avian; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                    1 ATTITACCTGATGATCCAGACAAGAAACCCCAGGCAAAGCAGCTACAGACCCAAGAAACCC
                                                                                                                                                                                       ;
0
                                                                                                                                                       Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avian chromodomain-helicase-DNA binding genes determine sex
birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                       Indels
                                                                                                                                                     DB 18;
                                                                                                         Sequence 153 BP; 61 A; 37 C; 27 G; 28 T; 0 other;
                                                                                                                                                       Score 102.4; DB 1
Pred. No. 4.8e-22;
                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                              121 GCAAGAAAGGAAGCACAAAAGGCTTGCTGGTGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicken CHD-W gene (partial sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        H.
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                                                                                                                                                     66.98;
79.68;
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                                                                                                                                                                                       121; Conservative
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                                                                                                                                                       Ouery Match
Best Local Similarity
Matches 121; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT42754;
                                                                               progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHD-W;
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                                                                                                                                                                                                                                                                                                                                                                ds; human; telomere repeat binding factor; A-TRF; dimerisation domain; telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
                                                                              52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAAT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, use to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                ö
                                                                                                                                             Score 92.4; DB 18;
Pred. No. 1.1e-18;
0; Mismatches 6;
                                                                                                                             AAAGACCTTGCAAGAAAGGAAGCACAAAGGCTTGCTGGTGCA
                                                                                                                                                                                                                                                                                                                                  Altered telomere repeat binding factor 1 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/product= "A-TRF"
                                                                                                                                                                                                                                      AAV59280 standard; cDNA; 1311
60.4%;
llarity 94.1%;
Conservative (
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97US-0800264
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Synthetic.
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 Query Match
Best Local Simi
Matches 96;
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Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;

Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;

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200005 - 0241825
200005 - 02461825
200005 - 0246474
200005 - 0246475
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2000US-0249215.
2000US-0249216.
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2000US-0232081.
2000US-0231968.
2000US-0232397.
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06-SEP-2000

06-SEP-2000

08-SEP-2000

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08-SEP-2000

09-SEP-2000

14-SEP-2000

14-SEP-2000

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16-SEP-2000

17-SEP-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, digestive system antigen; gene therapy, cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ss.
                                                                      Gaps
                                                                                                                                     52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTA 105
                                                                         ;
0
                  28.0%; Score 42.8; DB 19; Length 1311; 87.0%; Pred. No. 0.0016; Live 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                              Human digestive system antigen coding sequence SEQ ID NO: 1198
                                                                                                                                                                                                                                                                           AAK88882 standard; cDNA; 421 BP
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2000US-0180628.
2000US-0184664.
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2000US-0189874
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                            Best Local Similarity 87.03
Matches 47; Conservative
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                            Query Match
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2001WO-US01350
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2000US-0190076
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2000US-0214886.
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2000US-0217487.
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2000US-0230438
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2000US-0232401.
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                 WO200155350-A1
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02-MAR - 2000;
16-MAR - 2000;
18-APR - 2000;
19-MAY - 2000;
07-JUN - 2000;
30-JUN - 2000;
07-JUL - 2000;
11-JUL - 2000;
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14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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14-AUG-2000;
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22-AUG-2000;
23-AUG-2000;
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26-SEP-2000;
27-SEP-2000;
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22-AUG-2000;
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01-SEP-2000;
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14-SEP-2000;
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14-SEP-2000;
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14-SEP-2000;
                                                  02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendictly, Hirschsprung's disease, chronic colliss or ulcerative collis. The present sequence is a cDNA encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; colorectal cancer; colorectal cancer antigen; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 aaaaagcctcaggggaagcagctacagacccgagcggattacttgttgaagctgctcaga 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38.2; DB 22; Length 421;
Pred. No. 0.03;
0; Mismatches 28; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 421 BP; 148 A; 78 C; 127 G; 61 T; 7 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1198; 986pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 AAAGACCTTGCAAGAAAGGAAGC 134
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66.3%;
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                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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2000US-0256719
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2000US-0251856
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2000US-0249297
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Best Local Similarity 66.3
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                        Isolated polypeptide for treating, preventing and/or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAAT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%; Score 38.2; DB 22; Length 421; 66.3%; Pred. No. 0.03; tive 0; Mismatches 28; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO: 67; 522pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 AAAGACCTTGCAAGAAAGGAAGC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL06443 standard; cDNA; 6240 BP.
    Ruben SM;
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L1-JUL-2000; 2000US-0614150.
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Rosen CA, Barash SC,
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                                                                    WPI; 2001-457727/49.
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P-PSDB; ABB62340.
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Best Local Similarity
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ABL06443
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AAS51571 standard; DNA; 1269 BP.
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2000US-207727P.
2000US-242578P.
2000US-233625P.
2000US-257931P.
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ilarity 71.6%;
Conservative
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antibacterial;
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(ABB57737-ABB72072)
                                                                                                Query Match
Best Local Similarity
Matches 48; Conserv
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22-DEC-2000;
16-FEB-2001;
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26-MAY-2000;
23-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                  13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                             antibiotic;
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                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insectiodes, therapeutics in higher eukaryotes for the development of insectiodes, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL018176) and the encoded proteins
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                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster expressed polynucleotide SEQ ID NO 13808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental biology; cell signalling; insecticide;
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0
                                                                                                                                                                                               Length 6240;
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                                                                                                                                                          Sequence 6240 BP; 1675 A; 1682 C; 1760 G; 1123 T; 0 other;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                              DB 23;
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                                                                                                                                                                                             Score 36.6; DB Pred. No. 0.21; 0; Mismatches
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71.6%;
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11-JUL-2000; 2000US-0614150.
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                                                                                               (ABB57737-ABB72072).
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                                                                                                                                                                                                          Local Similarity
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Matches
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAATAAA 114
                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa DNA for cellular proliferation protein #156.
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0
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                                                                                                                                           Sequence 9933 BP; 2711 A; 2468 C; 2538 G; 2216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cellular proliferation gene; drug design.
                                                                                                                                                                                                                                                        23;
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                                                                                                                                                                                                                                                Score 36.6; DB Pred. No. 0.24; 0; Mismatches
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Human prostate-specific membrane antibody protein 12 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumour, haemopathy, HIV infection, immunological diseases and various
                   Human; ss; prostate-specific membrane antibody protein 12; cytostat: virucidal; immunomodulatory; antiinflammatory; hambactory; backettic; cancer; hambacpathy; human immunodeficiency virus infection; HIV; immunological disease; inflammation; prostate carcinoma; benign prostate tumour; metabolic disease; folic acid deficiency; neuropolic disease; folic acid deficiency; neuropolychosis; developmental disturbance.
                                                                                                                                                                                                                                              Human cDNA encoding prostate-specific membrane antibody protein 12.
    37 AAGCAGCTACAGACCCAAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
                                                                                                                               AAS15676 standard; cDNA; 1290
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P-PSDB; AAU10288.
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The proteins can be used to screen compounds in rational drug discovery programmes. The antisense uncleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic callular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes the human male enhanced antigen-2 (MEA-2). The present invention also described an antibody specific for the MEA-2 protein. The antibody can be used for the identification of a gene causing diseases related to spermatogenesis. The MEA-2 nucleotide sequence is useful as a chromosome marker, and in the detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; male enhanced antigen-2; MEA-2; identification; spermatogenesis;
spermatogenesis disease; chromosome marker; pancreatic cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human male enhanced antigen-2 (MEA-2) nucleotide sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                   17 CAGACAAGAAACCCCAGGCAAAGCAGCTACAGAACCAAGAAACCCCAGGCAAAGCAGCTAC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A new protein, human male-enhanced antigen-2, useful for detecting spermatogenesis diseases
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0
                                                                                                                                                                                                                                       Score 32.4; DB 23; Length 1269;
Pred. No. 2.5;
0; Mismatches 26; Indels 0;
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                                                                                                                                                                                     Sequence 1269 BP; 135 A; 436 C; 436 G; 262 T; 0 other;
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Pred. No. 5.8;
0; Mismatches 17;
                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 10-11; 21pp; Japanese.
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ilarity 71.2%;
Conservative (
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ilarity 64.9%;
Conservative
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P-PSDB; AAB69070.
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Best Local Similarity
Matches 42; Conserv
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Best Local Similarity
Matches 48; Conserv
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"Prostate-specific membrane antibody

protein 12"

/*tag= a /product=

AAF325(

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Location/Qualifiers 965..1288

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The invention relates to an isolated polypeptide of human prostate-specific membrane antibody protein 12 its fragment, analogue, derivative and nucleic acid encoding it. The polypeptide, nucleic acid encoding it and an antibody raised against it are applicable in diagnosis and treatment of cancer, hamenopathy, HIV (human immunodeficiency virus) infection, immunological diseases, various inflammations including, carcinoma of the prostate and benign tumour of the prostate, diseases due to metabolic defect of folic acid, neuropsychosis and developmental disturbance. The present sequence encodes the prostate-specific membrane antibody protein 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TTTTACCTGATGATCCAGACAAGAAACCCCAGGCAAAGCAGCTACAGACCCAAGAAACCCC 61
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llarity 54.3%; Pred. No. 5.8;
Conservative 0; Mismatches 53;
Claim 6; Page 30; 35pp; Chinese.
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Matches 63; Conserv
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Job time: 25931 sec

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
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62 AGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAATAAAGAC 117
                 Drosophila melanogaster expressed polynucleotide SEQ ID NO 34595.
                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
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64.8%;
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                       Drosophila melanogaster.
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Best Local Similarity
Matches 46; Conserv
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Search completed: August 2, 2002, 20:47:20

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: August 2, 2002, 16:52:12 ; Search time 8940.62 Seconds (Without alignments) 230.972 Million cell updates/sec
Title: US-08-973-363-3 Perfect score: 153 Sequence: 1 ATTTACCTGATGATCCAGACACAAAGGCTTGCTGGTGCA 153
Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414
Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database : EST:* 1: em_estba:* 2: em_estbum:* 3: em_estbum:* 4: em_estbu:* 5: em_estcv:* 6: em_estcv:* 7: em_estcv:* 17: em_estcv:* 10: qb_estc:* 11: qb_htc:* 11: qb_htc:* 12: em_gss_hum:* 13: em_gss_hum:* 14: em_gss_hum:* 15: em_gss_pln:* 16: em_gss_pln:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Descrit							SUMMARIES	
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7.7.7.7.7.7.7.8.8.8.8.8.8.8.8.8.8.9.0.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2	AL659353 AL659353 AL659353 AL659353 AL659353 AL659353 AL659353 AL659353 BET. BET. BET. BET. BET. BET. BET. BET.	119 a
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/organism="Silurana tropicalis"

/db_xref="taxon:8364"

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                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: LiEId12.plc
Sequencing primer: PlC
This sequence is from a Xenopus Gene Collection (XGC) library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
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                             Score 70; DB 9; Length 555
Pred. No. 3.5e-09;
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Pred. No. 3.5e-09;
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                                                                                                         0; Mismatches
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Location/Qualifiers
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80.4%;
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Silurana tropicalis
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PENNITON BEL55356 KRNS full-learing enriched, 16 days neconate thymus Mus musculus cDNA clond Al3004Life 3 similar to L00410 Mouse DNA-binding procesh (GHP-1) mRNA, mRNA sequence.

BEL5352 C 1:1626824

RENEWER MISSISSE C 1:1626824

RENEWER WORK ALT AND ALABASA T. F. TANIORA T. F. BARAA. R. SERVAL T. SERVA
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Euteleostomi, Amamalia, Euteleostomi, Alease, 1 to 660)

Arakwa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Takakashi, T., Sogabe, Y., Suzuki, H., Muramatsu, M., and Hayashizaki, Y., Tarkeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y., Tanaka, T., Toya, T., RIKEN Wolse ESTS (Arakawa, T., 'et al. 2001)
                                                                                            BB461065
BB461065 RIKEN full-length enriched, 12 days embryo spinal ganglion Wus musculus CDNA clone D130070B13 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
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URL.htp://genome.gsc.riken.go.jp,
Carninoi,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
AM., Konno,M.,
Onazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Mormalization and subtraction of cap-trapper-selected CDNAs to
prepare full-length CDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi,K., Eujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
On Jul 21, 2000 this sequence version replaced gi:9356558.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Tokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81,455,503-9222
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Pred. No. 1.8e-08;
0; Mismatches 21; Indels
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BB461065.2 GI:16426612
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79.28;
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hes 80; Conservative
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Mus musculus
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g ò RIKEN integrated sequence analysis (RISA) system--384-format

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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,K., Itoh,M., Rawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared of Renome Sequences Mamm. Genome .12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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DEF2P313J1040_r1 313 (synonym: hlcc2) Homo sapiens CDNA clone
DEF2P313J1040_r1 313 (synonym: hlcc2) Homo sapiens CDNA clone
DEF2P313J1040 5', mRNA sequence.
sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y. Computer-based methods for the mouse full-length CDNA
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                                                                                                                                                                                                                                                                      CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Encyclopedia Project of Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1. Similarity 79.2%; Pred. No. 1.8e-08;
80; Conservative 0; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tunor Gene Index
Unpublished (1997)

Unpublished (1997)

Email: cgapbs-remail.nlh.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                     Ltd.,
of the
           Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                           EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 547)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                               Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2): Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (NRTis): Research Centre for Biotechnology Ltd
Braunschweig/Germany) within the CDNA sequencing consortium of t
                                                                                                                                                                                                                                                                                                               No. 31 sequence available.
This clone (DKEZp313J1040) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANY: Email: clone@rzpd.de.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="kbrzpg1331040"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62.8; DB 9;
Pred. No. 3.1e-07;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 AGAGATCTTGCAAAAAAGAAGCTCTTTCTGGTGCGGG 336
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Best Local Similarity 77.6%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                 German Genome Project
                                                                                                                       Contact: Bloecker H
(bases 1 to 430)
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C
                                                                                                   Unpublished (1999)
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                                                                                 Wiemann,S.
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                 AUTHORS
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/organism="Homo sapiens"
/drawson:9606"
/db.zref="taxon:9606"
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/tissue_type="moderately_differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pcWV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF239967 821 bp mRNA linear EST 14-NOV-2000 601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone=lin=NuHAGE_1313129
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/inche="Yogan: bone marrow, Vector: pDNR-LIB (Clontech);
/incle="Yogan: bone marrow," Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); bouble-stranded cDNA was prepared from cell line RNA.
5 and 3' adaptors were used in cloning as follows: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 821)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.k column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAAT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.0%; Score 62.8; DB 9; Length 547; 77.6%; Pred. No. 3.2e-07; Live 0; Mismatches 22; Indels
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www-bio.llnl.gov/bbrp/image/image.html rnsert Length: 1924 Std Error: 0.00 Seg primer: -400P from Gibco High quality sequence, stop: 418.
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Location/Qualifiers
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Homo sapiens
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JOURNAL
COMMENT
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KEYWORDS
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Saito,K., Yamanoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
.Y., Suyano,S., Isogai,T.)
Unpublished (2000)
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGGCGGCAGATG-dT(30)BN-3' (where B = A, C, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboractics (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamaala; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 86)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
                                                                                                                                                                                                                                                                                                                        52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAAT 111
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                                                                                                                                                                                                                                        41.0%; Score 62.8; DB 10; Length 821; 77.6%; Pred. No. 3.5e-07; tive 0; Mismatches 22; Indels 0;
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Genomics Labbratora
Helix Research Institute
1512-3 Yana, Kisarazu, Chiba 292-0812, Japan
121 81-438-52-3951
Fax: 81-438-52-955
                                                                                                                                                                                                                                                                                                                                                                                                                                      69 AGAGATCTTGCAAAAAAGAAGCTCTTTCTGGTGCGG 106
                                                                                                                                                                                                                                                                                                                                                                                                             112 AAAGACCTTGCAAGAAAGGAAGCACAAAGGCTTGCTGG 149
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precursor cells"
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AU125712.1 GI:10950428
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                                                                                                                                                                                                                                                                                76; Conservative
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HRI human
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AU125712
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutherlia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1028)

8 NIH-MGC http://mgc.nci.nih.gov/.

1 (bases 1 to 1028)

2 (contact: Robert Strausberg, Ph.D.

2 (Email: Robert Strausberg, Ph.D.

2 (Email: Capabs-remail.nih.gov/

2 (Email: Capabs-remail.nih.gov/

2 (Email: Capabs-remail.nih.gov/

3 (Email: Capabs-remail.nih.gov/

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE895133 1028 bp mRNA linear EST 20-OCT-2000 601436060Fl NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3921087 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="melanotic melanoma"
//lab_host="melanotic melanoma"
//lab_host="milanotic proper resistant)"
//note="Organ: skin; Vector: pcMV-SpORT6; Site_1: NotI:
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

a 205 238 g 198 t
52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAAT 111
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41.0%; Score 62.8; DB 10; Length 1028;
Best Local Similarity 77.6%; Pred. No. 3.6e-07;
Matches 76; Conservative 0; Mismatches 22; Indels 0;
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/db_xref="taxon:9606"
/clone="IMAGE:3921087"
/clone_lib="NIH_MGC_72"
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BB834922.1 GI:17013165
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BE895133.1 GI:10358221
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EST 05-JUN-2000

9

ORGANISM

KEYWORDS

REFERENCE

AUTHORS

JOURNAL

COMMENT

TITLE

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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/dev_stage="Adult"
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Site_l: Smal; A mini-library was made by cloning products
Site_l: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BNO047-150 Seq primer: puc 18 forward High quality sequence start: 19 High quality sequence start: 19 Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 686)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
Simpson,A.J.
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              AW99/058
QV3-BN0047-150400-152-c03 BN0047 Homo sapiens CDNA, mRNA sequence.
AW997058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 AGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAATA 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                              AW997058.1 GI:8257292
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COMMENT
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Contact: Yoshihide Hayashizaki
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URL:http://
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                                                                                                                                                                Mammalia: Butheria; Rodentia; Scurognath; Muriabe; Murinae; Mus. 1 (bases 1 to 446)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Takithayatsu,N., Hiramoto,R., Hiraoka,T., Hirozane,T., Imotani,K., Ishii, Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nabhi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watchiki,A., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.
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                                                                                Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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/cell_line="RCB-0527 Jyg-MC(B)"
99 c 108 g 100 t
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Pred. No. 9.7e-07;
0; Mismatches 25
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/clone="G930033J21"
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75.2%;
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Best Local Similarity 75.2
Matches 76; Conservative
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Submitted (12-ARR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetracoon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracoon.
                                                            CNS04DVG 856 bp DNA linear GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 103K08 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Nocleostei; Acanthomorpha: Acanthopterygii; Teleostei; Buteleostei; Nocleostei; Tetracdontidae; Tetracdonio.

1 (bases 1 to 856)

1 (bases Lcrollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
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similar to SW:CHD2_HUMAN O14647 CHROMODOMAIN-HELICASE-DNA-BINDING
PROTEIN 2 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Genoscope sequence ID : C0BG103BF04LP1-end : T7" 308 c 252 g 206 t 6 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Tetraodon nigroviridis"
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/clone="103K08"
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GSS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-resegasc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
M., Konno.H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of Capt-trapper-selected cDNAs to
prepare full:length cDNA libraries for rapid discovery of new
genes. Genome-Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Toawa,M., Ohara,E.,
WatchAli,M., Yoneda,Y., Ishkkawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawahi,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKBN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
10 (11), 1757-1771 (2000)
v and Hayashizaki,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                  Eukaryota' Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutherta; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 438)

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiranoto,K., Hiraoka,T., Hiraoka,T., Hiraoka,T., Mordan,M., Matauyana,T., Y., Ito,M., Kawai,J., Kojima,Y., Kono,H., Kouda,M., Matauyana,T., Xi, Ito,M., Kawai,J., Kojima,Y., Kono,H., Kouda,M., Matauyana,T., Shalto,R., Sakai,C., Sakai,K., Sakazuei,N., Sasaki,D., Sato,K., Salto,R., Sakai,C., Sakai,K., Sakaume,N., Sasaki,D., Sato,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tamaka,T., Tomaru,A., Toparu,M., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihidé Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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RCB-0527 Jyg-WC(B) cDNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
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                           Cyprinidae; Danio,
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'Cyprinides, Danio.
'Cyprinides, Danio.
'I (bases 1 to 532)
'Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy , S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood , K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Wash Zebrafish EST Project 1998
L. Unpublished (1998)
Other ESTs: fq17e05, yl
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
                                                                                                                                                                                                                                                                                                                                                                                                         Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Info@enomesystems.com) and Research Genetics, Hubitsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
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/note="vector: pZIPLOX; Site_1: NotI: Site_2: SalI;
/note="vector: pZIPLOX; Site_1: NotI: Site_2: SalI;
/notional library was constructed in lambdaZIPLOX. Mass excision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."
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WashU Zebrafish EST Project 1998
Uppublished (1998)
Other_ESTS: f77409.y1
Other_ESTS: f77409.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
Fax: 314 286 1810
Email: zbraffsh@watson.wustl.edu
CDNA Library Preparation: John Wgai. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact:
info@genomesystems.com) and Research Genetics: info@resgen.com) and
RessourcententumPrimarDatenbank, Berlin, Germany (web address:
1 (bases 1 to 574)
Clark M. Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
Clark M., Johnson, S.L., Lehrach, H., Lee, R., Wylie, T., Underwood
K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swallar, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, B.,
and Milson, R., Materston, R.
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/sex="mixed male and female"
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/tissue_type="brain"
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/note="vector: pzIPLOX; Site_1: Not1; Site_2: Sal1;
/note="vector: pzIPLOX; Site_1: Not1; Site_2: Sal1;
/notinal library was constructed in lambdazIPLOX. Mexcision of the cDNA library was performed to yield pzIPLOX plasmids. Insert check was done in original library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó;
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Pred. No. 0.0042;
0; Mismatches 22; Indels 0;
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/organism="Danio rerio"
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/clone="5413937"
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Location/Qualifiers
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Seq primer: T7 from Gibco
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Best Local Similarity 73.5%;
Matches 61; Conservative
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24. (SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1993.DAT: *
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                                                                                                                     2, 2002, 20:47:20 ; Search time 1205.34 Seconds (without alignments) 217.937 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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			Description	Chick CHD-W dene t	Chick CHD-1A gene	Great tit CHD-W qe	Mouse CHD-1 gene (Chicken CHD-W gene	Chicken CHD-1A gen	Altered telomere r	Human digestive sy	Human colorectal c
SUMMARIES			n	AAT42/58	AAT42757	AAT42759	AAT42756	AAT42754	AAT42751	AAV59280	AAK88882	AAI57603
			DB	 FR	18	18	18	18	18	19	22	22
		Query	Length	 133	153	153	153	1316	6608	1311	421	421
	dР	Query	Match	700.0	91.6	88.5	0.69	65.6	62.1	26.9	25.9	25.9
			Score	 103	140.2	135.4	105.6	100.4	95	41.2	39.6	39.6
		Result	NO.	 -	7	m	. ₹	ស	9	7	æ	6

Drosophila melanog Prosophila melanog Prosophila melanog Proslectin ligand. Proslectin ligand. Human glycoprotein CDNA encoding a P- Human Proslectin l Human Proslectin l Human placenta P-s Proslectin ligand. Proslectin ligand. Proslectin ligand.	Soluble P-selectin Human P selectin I Human P selectin I Human P selectin I I P-selectin I I I Human I I I I I Human P selectin I Human P selectin I Human P selectin I Human Dwadenosin Human adenosin P-selectin I I P-selectin I I I P-selectin I I I I I I I I I I I I I I I I I I I		case-DNA binding 1; repeat of bases 22-51 the translated amino n in Fig 3"	
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	20000000000000000000000000000000000000	tandard tandard 7 (fir W gene		96 95 1NNC
		in ch i	de HD-	5-A1, 996; 996; 195;
mm		T 1 758 AAT42758 : AAT42758; 12-MAR-19: Chick CHD	rd; se D-1A; llus s y sc_dif	709639505 12-DEC-19 05-JUN-19 06-JUN-19 (ISIS-) I
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Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT47757), chicken CHD-W W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT47751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATTTTACCTGATGATCCAGATAAGAAACCCCAGGCTAAGCAGTTACAGACCAAGAAACCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 attitaccigatgatccagacaagaaaccccaggcaaagcagctacagaccaagaaaccc 60
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                                                                                                                                                                                                                                                                                                                                                                   DB 18; Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird; sex determination; chromodomain-Helicase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss.
                                                        Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                                                 Query Match 91.6%; Score 140.2; DB 18; Best Local Similarity 94.8%; Pred. No. 7.5e-36; Matches 145; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                            Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GCAAGAAAGGAAGCACAGAGACTTGCTGGTGCA 153
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52..81
                                                                                                           Claim 8; Fig 3; 76pp; English.
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 WPI; 1997-043127/04.
P-PSDB; AAW08147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758), and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/note= "bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                        Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 153; DB 18; Length 153; 100.0%; Pred. No. 5.5e-40; Ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bird; sex determination; chromodomain-Helicase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                              Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAAGAAAGGAAGCACAGAGACTTGCTGGTGCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT42757 standard; DNA; 153 BP
                                                                                                                                             Claim 8; Fig 3; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..81
Tiwari
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misc_difference
 Griffiths R,
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AAT42757 RESULT

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The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CHF-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTT 120
                                                                                   Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW008146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42751) the CHD-W (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATTITACCTGATGATCCAGATAAGAAACCCCAGGCTAAGCAGTTACAGACCAAGAAACCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 attettecagatgatectgataaaaaaccacaagcaaaacagttacagaecaaaaaacca 60
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.0%; Score 105.6; DB 18; Length 153; Best Local Similarity 80.9%; Pred. No. 1.1e-24; Matches 123; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                         Sequence 153 BP; 61 A; 37 C; 27 G; 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GCAAGAAAGGAAGCACAGAGACTTGCTGGTGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT42754 standard; cDNA; 1316 BP
                                             Claim 8; Fig 3; 76pp; English.
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                                                                                                                                                                                                                      52 AAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 1111
                                                                                                                                                                                      Gaps
located on the W chromosome. Probes based on CHD-W and CHD-lA give a W chromosome-specific signal on hybridisation to genomic DNA of a mon-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                  Score 100.4; DB 18; Length 1316;
Pred. No. 1.1e-22;
); Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
                                                                                               Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
                                                                                                                                                                                                                                                                                                                      1219 aaagaccttgcaagaaaggaagcacagagacttgctggtgca 1260
                                                                                                                                                                                                                                                                                      112 AAAGACCTTGCAAGAAAGGAAGCACAGAGACTTGCTGGTGCA 153
                                                                                                                                                                                                                                                                                                      Location/Qualifiers 228..5390
                                                                                                                                                                                                                                                                                                                                                                                                      AAT42751 standard; cDNA; 6608 BP.
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                                                                                                                                                    65.6%;
99.0%;
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                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicken CHD-1A gene.
                                                                                                                                                                   Similarity
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Matches 101;
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                                                                                                                                                                                                                                                                                                                                                                                   telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
                                                                                  ds; human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                 CAAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAA 110
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
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    Length 6608;
                                  Indels
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                                                                                                                                                            4160 taaagaccttgcaagaaaggaagcacaaaggcttgctggtgca 4202
                                                                                                                              111 TAAAGACCTTGCAAGAAAGGAAGCACAGAGACTTGCTGGTGCA 153
 Score 95; DB 18; L
Pred. No. 1.1e-20;
0; Mismatches 5;
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62.1%;
95.1%;
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                                Conservative
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/*tag=
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                Similarity
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 Query Match
Best Local S:
Matches 98;
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05-SEP-2000; 20000US-0229513.
06-SEP-2000; 20000US-0231431.
08-SEP-2000; 20000US-0231443.
08-SEP-2000; 20000US-0231443.
08-SEP-2000; 2000US-0231444.
08-SEP-2000; 2000US-0231444.
08-SEP-2000; 2000US-023399.
14-SEP-2000; 2000US-023399.
15-SEP-2000; 2000US-023399.
16-SEP-2000; 2000US-023399.
17-SEP-2000; 2000US-023399.
18-SEP-2000; 2000US-023399.
19-SEP-2000; 2000US-023399.
19-SEP-2000; 2000US-023499.
11-SEP-2000; 2000US-023499.
11-SEP-2000US-023499.
11-SEP-2000; 2000US-023499.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ss.
                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human digestive system antigen coding sequence SEQ ID NO: 1198.
                               Query Match 26.9%; Score 41.2; DB 19; Length 1311; Best Local Similarity 85.2%; Pred. No. 0.0015; Matches 46; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                   AAK88882 standard; cDNA; 421 BP.
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2000US-0229509
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2000US-0231243.
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2000US-0231413.
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2000US-0232080.
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2000US-0198123
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2000US-0209467
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2000US-0215135.
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2000US-0217487.
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2000US-0218290.
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2000US-0224518
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2000US-0229509.
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12-MAR-2000)
11-MAR-2000)
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11-MAG-2000)
11-AUG-2000)
11-AU
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26-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colliss or ulcerative collis. The present sequence is a cDNA encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; colorectal cancer; colorectal cancer antigen; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 aaaaagcctcaggggaagcagctacagacccgagcggattacttgttgaagctgctcaga 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
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Pred. No. 0.0034;
0; Mismatches 34; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human colorectal cancer antigen cDNA SEQ ID NO: 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1198; 986pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC, Ruben SM
                                                                                                                                                                                                                          2000US-0251030.
2000US-0251988.
2000US-0256719.
                                                                                                                                        2000US-0249299.
2000US-0249300.
2000US-0250160.
2000US-0250391.
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2000US-0251856.
2000US-0251868.
2000US-0251869.
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Best Local Similarity 63.8%;
Matches 60; Conservative
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2000US-0251990.
                     2000US-0249218.
2000US-0249244.
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  2000US-0249217
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2000US-0249297
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P-PSDB; AAM93109.
                                                     17.NOV-2000;
17.NOV-2000;
17.NOV-2000;
17.NOV-2000;
17.NOV-2000;
17.NOV-2000;
01.DEC-2000;
05.DEC-2000;
06.DEC-2000;
06.DEC-2000;
08.DEC-2000;
08.DEC-2000;
08.DEC-2000;
08.DEC-2000;
08.DEC-2000;
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Ruben

Barash SC,

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(HUMA-) HUMAN GENOME SCI INC
22-58P-2000

23-58P-2000

23-58
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Note: The sequence data for this patent did not form part of the printed aspecification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                Isolated polypeptide for treating, preventing and/or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection \rm e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 AAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
                                                                                                                                                                                                                                                                                                                                                                                                  25.9%; Score 39.6; DB 22; Length 421;
63.8%; Pred. No. 0.0034;
Live 0; Mismatches 34; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                  Claim 1; SEQ ID NO: 67; 522pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                 Sequence 421 BP; 148 A; 78 C; 127 G; 61 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 AAAGACCTTGCAAGAAAGGAAGCACAGAGACTTG 145
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.9%
Best Local Similarity 63.8%
Matches 60; Conservative
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P-PSDB; ABB62340.
                               WPI; 2001-457727/49.
P-PSDB; AAM38625.
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Rosen CA,
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Homo sapiens
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Matches
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                                                                                         (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wew isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                     55 AAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                        Score 35; DB 23; Length 6240; Pred. No. 0.25;
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                                                                                                                                                      Sequence 6240 BP; 1675 A; 1682 C; 1760 G; 1123 T; 0 other;
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70.1%;
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                                                                                                                                                                                                                 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               ABL06442;
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(ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                              6745 aagccccaggccaagcagctgcagacgcgtgccgagtacctgctcaagatcatcaagaag 6804
                                                                                                                                                                                                                                                                                                                                                       55 AAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAA 114
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0
                                                                                                                                                                                                                                       Length 9933;
                                                                                                                                              Sequence 9933 BP; 2711 A; 2468 C; 2538 G; 2216 T; 0 other;
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P-selectin
                                                                                                                                                                                                                                                                                             20;
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alpha-1,3/alpha-1,4-fucosyltransferase; PACESOL;
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treating inflammatory disease characterised by
mediated inter:cellular adhesion
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                                                                                                                                                                                                                                    Score 35; DB 2
Pred. No. 0.3;
0; Mismatches
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1..1239
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                                                                                                                                                                                                                                    22.9%;
Local Similarity 70.1%;
les 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6805 aacgtgg 6811
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The present sequence encodes a human glycoprotein having P-selectin daving Pessent sequence encodes a human glycoprotein having PSL activity. The present invention describes a glycoprotein having PSL activity which comprises a carbohydrate and a protein. The protein includes amino acids 4.2 60 of AAW72695, but lacks the intracellular domain and optionally the transmembrane domain of mature PSL protein may be useful in treating conditions characterised by P- or PSL protein may be useful in treating conditions characterised by P- or CE E-selectin mediated intercellular adhesion. Such conditions include myocardial infarction, bacterial or vital infection, metastatic monitable sclerosis, disease, glomerulonephritis, glingivitis, conditions, inflammatory disorders, asthma, emphysema, thermal injury, multiple sclerosis, disease, glomerulonephritis, glingivitis, conditions, include sclerosis, disease, glomerulonephritis, glingivitis, conditions, include and create and cytokine-induced toxicity. The periodoritis, hamolytic uremic syndrome, uccardial injury, disease, necrotising enterocolitis, and cytokine-induced toxicity. The isolated PSL protein may be useful in organ transplant crejection. The isolated PSL may be used to treat hamodialysis and leukophoresis patients. Additionally, isolated PSL protein may be used itself as an antimerastatic agent. The isolated PSL may be used to treat hamodialysis and inhibitor of P- or E-selectin-mediated intercellular adhesion.
                                                                                                                                                                                                                                                                                                        Human; glycoprotein; P-selectin ligand protein; inflammatory disease; intracellular domain; E-selectin-mediated intercellular adhesion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soluble P-selectin ligand glycoprotein - with truncated protein sequence lacking intracellular domain
       Human glycoprotein P-selectin ligand protein encoding cDNA.
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Sako DS, Shaw G, Veldman GM;
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1..1239
                                                                                                                                   AAV67131 standard; cDNA; 1239 BP
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93US-0112608.
93WO-US10168.
94US-0235398.
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28-APR-1994;
30-SEP-1994;
07-JUN-1995;
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26-AUG-1993;
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                                                                                                                                                                            AAV67131;
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                                                                                             RESULT
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                                                                                                                                                       0; Gaps
                                                                                                                                                                                                27 ACCCCAGGCTAAGCAGTTACAGACCAAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGC 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel P-selectin ligand protein - useful as anti-inflammatory agent and to identify inhibitors of selectin-mediated inter:cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-selectin ligand; adhesin; cell adhesion; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.5%; Score 31.4; DB 16; Length 1239; 54.9%; Pred. No. 2.2; tive 0; Mismatches 51; Indels 0;
                                                                                                            20.5%; Score 31.4; DB 15; Length 1239; Alarity 54.9%; Pred. NO.2.2; Conservative 0; Mismatches 51; Indels 0;
                                                                                                                                                                                                                                                                                    87 AGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAGA 139
                                                                                                                                                                                                                                                                                                               87 AGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAGA 139
                                             Sequence 1239 BP; 298 A; 422 C; 327 G; 192 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 83-85; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT02485 standard; cDNA; 1239 BP
P-selectin ligand glycoprotein.
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94US-0235398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 54.99
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-selectin ligand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cumming D,
Veldman GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-403865/51.
                                                                                                                                   Similarity
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28-APR-1994;
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Matches 62
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The present sequence encodes a P-selectin ligand protein. The P-selectin ligand is a glycoprotein. The protein binds in a calcium-dependent manner to P-selectin which is present on the surface of cells. The p-selectin ligand can be used to treat a wide variety of conditions characterised by intercellular adhesion involving P-, E- or L-selectins, e.g. myocardial infarction, infections, metastasss, inflammation, Crohn's disease, and to prevent transplant rejection. It can also be used to raise specific antibody (useful therapeutically as inhibitors of adhesion or for immunodiagnosis of inflammation and cancer) or to screen for selective inhibitors. Fusion proteins of the P-selectin ligand protein are used to treat conditions related to selectin expression, e.g. fusion with interleukin-11 to treat bone marrow morphogenic protein (BMP) to stimulate bone or cartilage formation, or other cytokines to sites of inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                  P-selectin ligand protein; glycoprotein; human; calcium-dependent; intercellular adhesion; E-selectin; L-selectin; myocardial infarction; inflammation; Crohn's disease; transplant rejection; rejection; ss.
                                                                                                     525 accagcagccacggaagcacagaccactcaacccacaggcctggaggcacagaccactgc 584
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated DNA encoding fusion protein including P-selectin ligand fragment - to direct second component, e.g. cytokine, to sites of selectin expression, used e.g. to stimulate bone and cartilage
                                                                    27 ACCCCAGGCTAAGCAGTTACAGACCAAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGC 86
                                    ;
 Length 1239;
                                                                                                                                         87 AGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAGA 139
                                                                                                                                                                           585 accagcagccatggaggcacagaccactgcaccagcagccatggaagcacaga 637
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sako DS;
                                51;
   DB 19;
 Score 31.4; Di
Pred. No. 2.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Larsen GR,
                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding a P-selectin ligand protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 1.1239
                                                                                                                                                                                                                                                                AAV22850 standard; cDNA; 1239 BP
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   20.5%;
54.9%;
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                                    62; Conservative
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Veldman GM;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-AUG-1996;
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                                                                                                                                                                                                                                              Length 1239;
                                                                                                             Indels
               Sequence 1239 BP; 298 A; 423 C; 326 G; 192 T; 0 other;
                                                                     20.5%; Score 31.4; DB 19;
54.9%; Pred. No. 2.2;
ive 0; Mismatches 51;
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Matches 62; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description	BB155356 BB166105 BB461065 BB AL659353 AL654524 AL654524 AL664524 AL664524 BB83445275 WB125712 AL890775 WB125712 AL890775 WB125712 AL890775 GB184447 BB834447 BB8344447 BB834447 BB834447 BB834447 BB834447 BB834447 BB834447 BB8344447 BB834447 BB834447 BB834447 BB834447 BB834447 BB834447 BB8344447 BB834447 BB83447 BB834447 BB83447 BB834447 BB83447	1825 BM024825 fu73e09.x
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Score		46.2
Result No.	0 0 23 11 10 10	c 17

BM185005 fv16c08.x AW996787 0073-BM004 AL558477 AL528477 AL322625 Tetraodon AL329275 Tetraodon AL332812 Tetraodon AL333335 Tetraodon AL333335 Tetraodon AL3413505 Tetraodon AL3413505 Tetraodon AL341357 Tetraodon AL3413772 Tetraodon AL341668 Tetraodon AL317122 Tetraodon AL317122 Tetraodon AL317122 Tetraodon AL31668 Tetraodon AL35039 Tetraodon AL35039 Tetraodon AL35039 Tetraodon AL35039 Tetraodon	
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608 633.7 633.7 608.3 608.	
2009999 2009999 20099999999999999999999	00000000
44 4 4444444 445.0000 445.00000 445.0000000000	
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ALIGNMENTS

BB155356 RIKEN full-length enriched, 16 days neonate thymus Mus BB155356 RIKEN full-length enriched, 16 days neonate thymus Mus DNA-bloding protein (CHD-1) mRNA, mRNA sequence. BB155356 GI:16268254	house mouse. Mus musculus Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases ! to 619) Arakawa T., Carninol, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda M., Koya, S., Matsuyama, T., Migazaki, A., Nomura, K., Ohno, M., Ökazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki D., Shibata, K., Shinaqawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,	FIREN MOUSE ESTS (AZRAWA), T., et al. 2001) Unpublished (2001) Use (2000 this sequence version replaced gi:8811286. Contact: Yoshihide Hayashiaski Laboratory for denome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) Tel: 81-45-503-922 Fax: 81-45-503-923 Fax: 81-45-503-922 Fax: 81-45-503-923 Fax: 81-4	wayı, r rujimane, S., inoue, R., ioyama, F., iozawa, K., Tanaka, T., Matsuura Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
RESULT 1 BB155356 LOCUS DEFINITION ACCESSION VERSION KRYMODIS	SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL COMMENT	

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"Hiramoto,K., Hori,F., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
"Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
"M., Koya,S., Masusyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,K., Ohno,M.,
Tagami,M., Tagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
On Jul 21, 2000 this sequence version replaced gi:9356558.
Contact: Yoshihide Hayashizaki and Chenical Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
Fax: 81-45-503-9226
Fmail. Gonome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.go.jp,

Carlinol.p., Shibata,Y.,

Carlinol.p., Shibata,Y., Hayatsu,M. and Hayashizaki,Y.

Carlinol.p., Shibata,Y., Hayatsu,M. and Hayashizaki,Y.

Mormalization and subtraction of cap-trapper-selected cDNas to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. . 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,M., Tanaka,T., Matsuura

S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

Hayashizaki,Y.

KRIEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itch,M., Carninci,P., Sugahara

Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)

Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa

Hayashizaki,Y.

K., Fukuda,S., Hara,A., Itch,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCGCGCCAACTCGAGTTTTTTTTTTTTTVN 3'], cDNA was
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                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/db_xef="taxon:10090"
/clone="D130070813"
/clone_lib="RIKEN full-length enriched, 12 days embryo
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
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/tissuc_type="spinal ganglion"
/dev_stage="12 days embryo"
/lab_host="DHIOB"
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                                                                                                                                                                                                          REFERENCE
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                                    KEYWORDS
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VERSION
                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)

Konno, H., Evkunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB461065 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130070B13 3' similar to L10410 Mouse BB461065 BDNA-binding protein (CHD-1) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                             encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Rawai, J., Shibata, K. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/clone_lib="RIKEN full-length enriched, 16 days neonate
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 AAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
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Pred. No. 5.9e-10;
0; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="thymus"
/dev_stage="16 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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80.2%;
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118 c
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source

FEATURES

Query Match

Matches

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LOCUS

BB461065

RESULT

ACCESSION

BASE COUNT

154

Mon Aug

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112 AAAGACCTTGCAAGAAAGGAAGCACAGAGACTTGCTGGTGCA 153
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BB834922.1 GI:17013165
                                                                                                                                                                                                                                                                                                                                                                                  AL644594.1 GI:16796719
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Best Local 9
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ORGANISM
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JOURNAL
COMMENT
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AL644594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 AAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tropésangér.ac.uk
Sanger Xenopus tropécals EST project 2001
Sanger Xenopus tropécals EST project 2001
TROPECALIS.SEQUENCE.ID: TNeu045e20.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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1 (Bases 1 to 593)

Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.7%; Score 66.8; DB 9; Length 593; 78.4%; Pred. No. 2.5e-09; tive 0; Mismatches 22; Indels (
                                                                                                                                                                                                                                                                                                                                                ch 45.1%; Score 69; DB 9; Length 660; B 1 Similarity 40.2%; Pred. No. 5.9e-10; S.9e-10; 81; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 AAAGACCTTGCAAGAAAGGAAGCACAGAGACTTGCTGGTGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="INeu045e20"
/clone=lib="XGC-neurula"
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Matches 80; Conservative
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Best Local Similarity
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ORIGIN
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AUTHORS
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JOURNAL
COMMENT
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KEYWORDS
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BBB34922 REEN full-length enriched, mammary gland RCB-0527
BBB34922 RIKEN full-length enriched, mammary gland RCB-0527
JYG-WC(B) CDNA Mus musculus CDNA clone G930033321 3', mRNA
                                                                                                                                                                           AL644594 AGC-egg Silurana tropicalis CDNA clone L1E1d12 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="egg".s?
/dev_stage="egg".s?
/lab_host="Escherichia coli XLl-blue"
/note="vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
/note="vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCS107 with
ECORI at the 5' end and NotI at the 3' end*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
Mus musculus
Euka musculus (chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                              western clawed frog.
Silurana tropicalis
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Localifiers
1. 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xehopodinae; Silurana.
1 (bases 1 to 64).
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (10_2001) (upublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.7%; Score 66.8; DB 9; Length 645; 78.4%; Pred. No. 2.6e-09; tive 0; Mismatches 22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tropésanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: L1E1d12.plc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="LiEid12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinxton, Cambridgeshire, CB10 15A, UK
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FEATURES

us-08-973-363-4.rst

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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wm95fil.xl NCL_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443725 3' similar to SW:CHDL_HUMAN O14646 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1; mRNA sequence.
A1890775.
A1890775.1 GI:5595939
                                                                                                                                                                                                                                                                                                                                                                                                             Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2): Email s. Wiemann@dkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
                                                                                                                                                                                                                          Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 547)
                                                                                                                                            Chordata, Craniata, Vertebrata, Euteleostomi,
Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                            ,S.
EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone (DKFZp313J1040) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 AAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .430
/organism="Homo sapiens"
/db_xref="Laxon:9606"
/clone="DRE2231311040"
/clone=lib="313 (synonym: hlcc2)"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61.2; DB 9;
Pred. No. 1e-07;
0; Mismatches 23;
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Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
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           AL601246
AL601246.1 GI:15164752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 76.5%;
Matches 75; Conservative (
                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 430)
                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
C
                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Exploratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Vokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9212
Fax: 81-45-503-9216
Email: genome-reségsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,M., Tnoue,Y., Kira,A. and
Hayashizaki,Y., Putzaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 446)
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,
Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Oktazaki,Y., Okido,T.,
Salto,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takakashi,F., Takaku-Mahira,S., Tanakar,T., Tomaru,A., Toya,T.,
Watahiki,A., Yasunishi,A., Muramatsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
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Alo bp mRNA linear EST 14-AUG-2001
DKFZp313J1040_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DKFZp313J1040 5', mRNA sequence.
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/clone="699803373"
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RCB-0527 Jyg-MC(B) cDNA"
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                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Contact: Yoshihide Hayashizaki
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.,
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Www-bio.lnl.qov/Dorp/image/image/image.html
Insert Length: 1924 Std Error: 0.00
Seq Primer: -400P from Gibco.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: uterus; Vector: pCNV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012**
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MIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CONTACT: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Taball: egapbs-remail.nih.gov
Tissue Procurement: ArCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be thep://image.lni.gov
http://image.lni.gov
Plate: LiCMI033 row: k column: 18
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                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:2443725"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinome, 3 pooled tumors"
/lab_host="DH10B"
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High quality sequence stop: 562.
Location/Qualifiers
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/db_xref="taxon:9606"
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Isogal,T.

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HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishli,S., Salto,K., Yamamoto,J., Nakamura,Y., Nishlikawa,T., Nagal,T., Suzuki,Y., Sugato,S., Isogal,T.)

L. Y., Sugano,S., Isogal,T.)

L. Contact: Takao Isogal

Genomics Laboratory

Hellx Research Institute

132.3 Yana, Kiasarau, Chiba 292-0812, Japan

Tel: 81-438-52-3951

Email: genomics@hri.c.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Hellx

Research Institute; CDNA hibrary construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Hellx Research Institute.
/clone_lib="NIH_MGC_S4"
//tissue_type="from chrontom yelogenous leukemia"
//tab_host="DHOB (T1 phage-resistant)"
//note="Organ chrontom vector: pDNR-LIB (Clontech);
//note="Organ bone marrow; Vector: policy bone marrow;
//note="Organ bone marrow; Vector: policy bone;
//note="Organ bone; Vector: policy bone; Verlage insert size 1.75 kb (range 0.94.0 kb). 15/15 colonies
//note: policy policy bone; Vector: policy bone;
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/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
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1 (bases 1 to 866)
1 (bases 1' wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AAAGACCTTGCAAGAAAGGAAGCACAGAGACTTGCTGG 149
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/clone_lib="NT2RM4"
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AU125712.1 GI:10950428
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Matches

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ORIGIN

DEFINITION

RESULT 1 BE895133

ACCESSION

VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yosohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
Email: genome-resegsc.riken.go.jp,
URL: http://genome-gsc.riken.go.jp,
URL: http://genome-gsc.riken.go.jp,
URL: http://genome-gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
URL: Anno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, M.
Normalization and subfortaction of Captrated
Schore, Matahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
/S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y., Shibata, K., Itch, M., Carninci, P., Sugahara
/Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length CDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 438) Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Tto, M., Kawai, J., Kojina, Y., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Osazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akhira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA"
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                                                BB830730 RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA Mus musculus cDNA clone G930013K04 3', mRNA
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Pred. No. 2.6e-06;
0; Mismatches 21;
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/db_xref="taxon:10090"
/clone="G930013K04"
                            438 bp
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Best Local Similarity 78.4
Matches 80; Conservative
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                                                                                                                                      ACCESSION
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KEYWORDS
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BB830730
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/tissue_type="melanotic melanoma"
/lab_host="Dpm"DB (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTP/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9753 row: h column: 16
High quality sequence stop: 488.
I. 1028
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NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                             Length 866;
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Pred. No. 1.2e-07;
                                                                             Score 61.2; DB 9;
Pred. No. 1.2e-07;
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_72"
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                                                                       ch 40.0%;
1 Similarity 76.5%;
75; Conservative
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GSS; genome survey sequence.

Fitzacdon nigroviridis.

Tetracdon nigroviridis.

Tetracdon nigroviridis.

Tetracdon nigroviridis.

Retaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostoml;

Actinopterygi; Neopterygii; Teleostel; Euteleostel; Neoteleostel;

Acanthomorpha: Acanthopterygii; Percomorpha: Tetracdontiformes;

Tetracdontidae; Tetracdon.

El (bases 1 to 856)

Sest-Crollius H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,

Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and

Weissenbach,U.

Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracodon nigroviridis

N. Oppulsiached
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Submitted (12-ARR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-ARR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                          CNSO4DVG 856 bp DNA linear GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 103KO8 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Bukaio rezia Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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6 others
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/db_xref="taxon:99883"
/clone="103K08"
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ilarity 69.4%; Pred. No. 2.5e-05;
Conservative 3; Mismatches 27;
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/note="Genoscope sequence ID
308 c 252 g 206 t
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BI844947.1 GI:15957470
                                                                                                                                                                        sequence.
AL286261
AL286261.1 GI:8024707
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Genoscope.
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Best Local Similarity
Matches 68; Conserv
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BI844947/c
LOCUS
DEFINITION
RESULT 13
CNSO4DVG/C
LOCUS
DEFINITION
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/dayxafe"=taxon:9606"
/clone_lib="BMO01"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: pucl8; Site_l: Smal;
/note="Organ: breast_normal; Vector: pucl8; Site_l: Smal; Vector: pucl8; Site_l: Smal;
/note="Organ: breast_normal; Vector: pucl8; Site_l: pucl8; Vector: pucl8; Site_l: pucl8; Vector: pucl8; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Josas I to 686)

Busas Neto, E., Garcia Correa,R., Verjovski-Almeida,S., Eriones,M.R., Magai,M.A., da Silva, W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpsoc@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BNO047-150
400-152-c031=x2000-04-158t4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stor:
Location/Oualifiers
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QV3-BN0047-150400-152-c03 BN0047 Homo sapiens cDNA, mRNA sequence.
AM997058
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. 17), 3491-3496 (2000)
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Pred. No. 1.2e-05;
0; Mismatches 13; Indels
                           AW997058.1 GI:8257292
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Best Local Similarity 82.7%;
Matches 62; Conservative
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Fax: +55-11-2707001
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                                                                l (bases 1 to 512)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: zbrafish@watson.wustl.edu
Usubn Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@esseyen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
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Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/db.morel_lib="readmisson" / db.morel_lib="readmisson" / develor="lib="readmisson" / develor
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                                                                                                                                                                                                                                                                                                    WashU Zebrafish EST Project 1998
Unpublished (1998)
Other_ESTS: fq17e05.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 0.0025;
0; Mismatches 23; Indels 0
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/organism="Danio rerio"
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High quality sequence stop: 1.
Location/Qualifiers
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daid wilson, K.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Other_ESTS: fY7409.91
Contact: Stephen L. Johnson
Washington University School of Medicine
Tel: 314 286 1800
Email: zbraffsh@watson.wustl.edu
CDNA Library Preparation: John Ngai. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.resgen.com) and Ressarch Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
Seq primer: T7 from Gibco
High quality sequence stop: 328.
Cyprinidae, Danio.

(Cyprinidae, Danio.

(Cyprinidae, Danio.

(Chases I to 574)

(Clark, M., Johnson, S.)

(Clark, M., Johnson, S.)

(Clark, M., Johnson, S.)

(Clark, M., Johnson, S.)

(Corresponding, M., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., and Wilson, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 574

/organism="Danio rerio"
/db_rate="taxon:7955"
/dlone="541337"
/clone="15="zebrafish adult brain"
/clone=lib="zebrafish adult brain"
/fissue_type="bain"
/fissue_type="bain"
/dev_stage="dault"
/lab_host="E. coli DH10B"
/note="vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
/note="vector: pZIPLOX; Insert check was done in original
//dev_stage="vector: pZIPLOX; Passmids: Insert check was done in original
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 AAGAAACCICAAGGAAAGCAGITACAGAIGCGAACAGACTACTIGCIGAAGAIGCIGAAG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 AAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46.2; DB 10;
Pred. No. 0.0026;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: August 2, 2002, 16:52:15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AAAGACCTTGCAAGAAAGGAAGC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.2%;
Best Local Similarity 72.3%;
Matches 60; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 c
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us-08-973-363-5.rng

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Great tit CHD-W de	Chick CHD-W gene f	Chick CHD-1A gene	Mouse CHD-1 gene (Chicken CHD-1A gen	Chicken CHD-W gene	Altered telomere r	Drosophila melanod	Drosophila melanog
SUMMARIES	· E	AAT42759	AAT42758	AAT42757	AAT42756	AAT42751	AAT42754	AAV59280	ABL06443	ABL06442
	DB	18	18	18	18	18	18	19	23	23
	Query Match Length DB	153	153	153	153	6608	1316	1311	6240	9933
ф	Query	0.66	87.5	85.4	0.69	57.9	57.3	28.0	22.9	22.9
	Score	151.4	133.8	130.6	105.6	88.6	87.6	42.8	35	32
	Result No.	н	7	Э	4	S	9	7	80	σ

(ISIS-) ISIS INNOVATION LTD.

Human digestive sy Human colorectal c Drosophila melanog Human CDNA encodin Human HBM gene reg Human HBM gene reg Listeria monocytog	Mana encount Novel Human secreted pro Human Secreted pro Human DA sequence Human neuregulin-1 Human neuregulin-1 Nucleotide sequenc	Human Inmune syste Human DNA for a no Human DNA for a no Mouse khos cDNA. Drosophila melanog	Nucleotide sequenc Drosophila melanog Drosophila melanog Human immune syste Human novel protei Human novel protei Human covel protei Human colon cancer	Human secreted pro Human secreted pro DNA encoding novel Human fiferential Human nervous syst Human reproductive Candida albicans e
AAK88882 AAI57603 ABI:16322 AAS15676 ABA82625 ABA82623 ABA82623	AASSUSS ABL34241 AAC19266 AAS94914 AAK95240 AAK96733 AAV90913	ABL33618 AAS31523 AAS31522 AAT62793 ABL23558	AAF84800 ABL15583 ABL33194 AAS61202 AAD16644 AAS26100 AAH34442	AAF3345 AAS01552 AAS86693 AAH81749 AAK51880 ABA18350 ABA107353 AAC07353
222222		25 25 27 23 23	222244332	55555355
421 421 34750 1290 66933 72049	11691 11691 461 2412 1503900 1503900	7238 13996 14001 2389 3150	110000 5274 8785 14861 14861 242 2618 2791	2791 2791 2965 5350 5359 11343 20746 1521
22444444	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			, , , , , , , , , , , , , , , , , , ,
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112 113 114 115 116	118 120 23 23 24 24 25	2002	333310 3343310 348310 348310	8 6 6 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6
O	00000	O	0 000 00	00 000

ALIGNMENTS

/*tag- a /note= "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3" Bird; sex determination; chromodomain-Hellcase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss. Location/Qualifiers 52..81 Great tit CHD-W gene fragment. 96WO-GB01341 95GB-0011439. 12-MAR-1997 (first entry) Key misc_difference 52 WO9639505-A1. 06-JUN-1995; 05-JUN-1996; 12-DEC-1996. Parus major. AAT42759; ţu

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Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT4757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759), and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                 1 ATTTTACCTGATGACCCCAGATAAGAAACCACAGGCAAAGCAGTTGCAGACCAAGAAACCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                              1 attttacctgatgatccagataagaaaccccaggctaagcagttacagaccaagaaaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
"bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex determination; chromodomain-Helicase-DNA binding 1;
                                               chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                 Score 133.8; DB 18;
Pred. No. 7.5e-31;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GCAAGAAAAAAGAAGTGCAAAGACTTACTGGTGCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHD-1A; CHD-W; W chromosome; ss.
                                                                                                 Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                              87.5%; 92.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chick CHD-1A gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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 WPI; 1997-043127/04.
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                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                 P-PSDB; AAW08148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW08147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT42757;
                                                 Avian
                                                                  birds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT42757
 Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chronosome) gene (AAT42758), and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT4774-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATTTTACCTGATGACCCAGATAAGAAACCACAGGCAAAGCAGTTGCAGACCAAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
                                                                             Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                             Score 151.4; DB 18; Length 153;
Pred. No. 4e-36;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                              Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAAGAAAGAAGTGCAAAGACTTACTGGTGCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT42758 standard; DNA; 153 BP
                                                                                                                            Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                           99.0%;
nilarity 99.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chick CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
Griffiths R, Tiwari
                             WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
misc_difference 52
                                              P-PSDB; AAW08149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT42758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
AAT42758
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Gaps

0

Indels

Length 153;

DB 18;

9

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Gaps

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Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-1W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAMW014649. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) checken also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The chicken CHD-W gene (AAT42754) acting alone or in conjunction with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 caagcaaaacagttacagacccgtgcagactacctcatcaaactacttagcagagatctt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATTTTACCTGATGACCCAGATAAGAAACCACAGGCAAAGCAGTTGCAGACCAAGAAACCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 69.0%; Score 105.6; DB 18; Length 153; Best Local Similarity 80.9%; Pred. No. 2.1e-22; Matches 123; Coonservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                 Sequence 153 BP; 61 A; 37 C; 27 G; 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GCAAGAAAGAAGTGCAAAGACTTACTGGTGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
228..5390
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT42751 standard; cDNA; 6608 BP
                                                 Claim 8; Fig 3; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 5; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-GB01341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chicken CHD-1A gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffiths R,
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                                                                                                                                                                                                                                                                                                                      progeny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                          Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAM42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-IA (see also AAT42754) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATTTTACCTGATGACCCAGATAAGAAACCACAGGCAAAGCAGTTGCAGAACCAAGAAACCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.4%; Score 130.6; DB 18; Length 153; 90.8%; Pred. No. 6.8e-30; Live 0; Mismatches 14; Indels 0;
                  Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Avian chromodomain-helicase-DNA binding genes determine sex in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bird; sex determination; chromodomain-Helicase DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GCAAGAAAGAAGTGCAAAGACTTACTGGTGCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse CHD-1 gene (bases 3855-977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT42756 standard; DNA; 153 BP
                                                                                               Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHD-1; CHD-W; W chromosome; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-GB01341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity yo.o.
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-043127/04.
P-PSDB; AAW08146.
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misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from a stage 10.12 chicken embryo cDNA is a clones isolated from a stage 10.12 chicken embryo cDNA ibrary using a great tit CHD-W sequence (see also AAT42755) as The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic
                                                                                                                                                                                                                                                                                                                                                                                              4100 caagaaaccccaggcaaagcagctacagacccgtgcagactacctcattaaattactgaa 4159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT47751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 1D-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-IA give a W chromosome specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W
                                                                                                                                                                                                                                                                                                                                                          51 CAAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAA 110
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex determination; chromodomain-Helicase-DNA binding 1 Avian; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                             bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                non-rarite bird and can be used for sex determin. of a bird. CHD nucleic acids can also be used to control the sex of progeny of a
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                                                                                                                                                                                                                                                                               57.9%; Score 88.6; DB 18; Length 6608; 91.3%; Pred. No. 7.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                      Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 TAAAGACCTTGCAAGAAAGAAGTGCAAAGACTTACTGGTGCA 153
                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicken CHD-W gene (partial sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT42754 standard; cDNA; 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9639505-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT42754;
                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bird;
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                                                                                                                                                                                                                                                                                                                                                             telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
                                                                       ds; human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                           52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, use to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                             ;
 Length 1316;
                             Indels
                                                                                                                                                1219 aaagaccttgcaagaaaggaagcacagagacttgctggtgca 1260
                                                                                                                  112 AAAGACCTTGCAAGAAAGAAGTGCAAAGACTTACTGGTGCA 153
Score 87.6; DB 18;
Pred. No. 9.8e-17;
                                                                                                                                                                                                                                                                                                                Altered telomere repeat binding factor 1 gene.
                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Steensel B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "A-TRF"
                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                         AAV59280 standard; cDNA; 1311
57.3%;
91.2%;
                                                                                                                                    98WO-US02765
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97US-0800264
                                                                                                                                                                                                                                                                                    (first entry)
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                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..1311
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               Similarity
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                                                                                                                                                                                                                                                                                    14-DEC-1998
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                             93;
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Query Match
Best Local Si
Matches 93;
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                      AAV59280;
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                                                                                                                                                                                                         AAV59280
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Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;

Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;

Drosophila melanogaster expressed polynucleotide SEQ ID NO 13808. Drosophila; developmental biology; cell signalling; insecticide;

ABL06442 standard; cDNA; 9933 BP

RESULT ABL06442

26-MAR-2002 (first entry)

ABL06442;

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pharmaceutical; gene; ss. Drosophila melanogaster.

WO200171042-A2.

27-SEP-2001.

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The sequence data for this patent did not form part of the printed appending the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811.
                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                        0;
                                                                                                                               52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTA 105
/ Match 28.0%; Score 42.8; DB 19; Length 1311; Local Similarity 87.0%; Pred. No. 0.0026; hes 47; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                     ABL06443 standard; cDNA; 6240 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                  ABL06443;
          Query Match
                                                                    Matches
                                                                                                                                                                                                                                                                                       RESULT
ABL06443
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                                                                                                                                                                                                                                                                                                                   55 AAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAA 114
                                                                                                                                                                                                                                                                                  Query Match 22.9%; Score 35; DB 23; Length 9933;-
Best Local Similarity 70.1%; Pred No.1; Assatches 47; Conservative 0; Mismatches 20; Indels 0; Gaps
                                                                                                                                                                                                                                                               Sequence 9933 BP; 2711 A; 2468 C; 2538 G; 2216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                   AAK88882 standard; cDNA; 421 BP.
                                                                                                                                                                                                                                                                                                                                                   6805 aacqtgg 6811
                                                                                                                                                                                                                                                                                                                                       115 GACCTTG 121
                                                                                                                                                                                                                                                                                                                                                                                                AAK88882;
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ID AAK8
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AC AAK8
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0; Gaps

55 AAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAA 114

4265 aacgtgg 4271

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115 GACCTTG 121

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Oubry Match 22.9%; Score 35; DB 23; Length 6240; Best Local Similarity 70.1%; Pred. No. 0.89; Matches 47; Conservative 0; Mismatches 20; Indels (

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention disciloses genomic DNA sequences (ABL01817, expressed DNA sequences (ABL01804 DAL16175) and the encoded proteins (ABB7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell

Li PWD, Myers EW;

Venter JC, Adams M, WPI; 2001-656860/75.

P-PSDB; ABB62339

interactions -

(PEKE) PE CORP NY.

23-MAR-2001; 2001WO-US09231. 23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150. Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.

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2000US-0235484
2000US-0235834
2000US-0235835
2000US-0236327
2000US-0236367
2000US-0236369
2000US-02363703
2000US-02363703
2000US-02363703
2000US-02363703
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2000US-0239935
2000US-0239935
2000US-0249937
2000US-0241785
2000US-0241785
2000US-0241786
2000US-0241786
2000US-0241786
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2000US-0246611.
2000US-0246613.
2000US-0249207.
2000US-0249208.
                2000US-0233064.
2000US-0233065.
2000US-0234223.
2000US-0234274.
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05-DEC-2000;
   Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ss.
                               Human digestive system antigen coding sequence SEQ ID NO: 1198
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                                                                                                                                                                                                                                                    Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.4%; Score 34.2; DB 22; Length 421; 64.6%; Pred. No. 0.71; tive 0; Mismatches 28; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 421 BP; 148 A; 78 C; 127 G; 61 T; 7 other;
                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1198; 986pp; English
                                                                                                                                                               Rosen CA, Barash SC, Ruben SM;
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08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0251990.
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2000US-0209467
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Matches 51; Conservative
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P-PSDB; AAM93109.
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52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
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                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 439.
                                                   Sequence 421 BP; 148 A; 78 C; 127 G; 61 T; 7 other;
         Note: The sequence data for this patent did not specification, but was obtained in electronic foat ftp.wipo.int/pub/published_pct_sequences.
                                                                                 Score 34.2; DB pred. No. 0.71; 0; Mismatches
                                                                                                                                                                                                                                        ABL16322 standard; DNA; 34750 BP.
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                                                                                 7 Match 22.4%;
Local Similarity 64.6%;
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis -
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P-PSDB; AAM38625.
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acid detection reagent for detecting 1000 or more a and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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DB 24; Length 1290;

Local Similarity

Query Match

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                                                                                                                                                    D 17588 ATAAAAAACTGTCATTGCTGTCGCCGGTATATAAGTAAATTAAATAGTGAATA 17529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ss; prostate-specific membrane antibody protein 12; cytostatic; virucidal; immunomodulatory; antibifammatory; haemostatic; cancer; heemopathy; human immunodefictency virus infection; HIV; immunodogical disease, inflammation; prostate carcinoms; benign prostate tumour; metabolic disease; folic acid deficiency; neuropsychosis; developmental disturbance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate-specific membrane antibody protein 12 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumour, haemopathy, HIV infection, immunological diseases and various inflammations
                                                                                                     53 AGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAATA 112
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA encoding prostate-specific membrane antibody protein 12.
                                      0;
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                             41; Indels
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                                                                                                                                                                                                                                                                                                113 AAGACCTTGCAAGAAAAGAAGTGCAAAGACTTACTGGTG 151
Best Local Similarity 58.6%; Pred. No. 4.4; Matches 58; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-2001; 2001WO-CN00351
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/product=
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The present invention describes the human Zmax1 gene and the high bone mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM genes have osteopathic activities. The genes can be used in gene therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoporosis, Paget's disease, sclerostosis, osteomalacia and fibrous dysplasia. ABA82038 to ABA82700 and ABG8188 to AAG68193 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTT 120
                                                                                                             766 ttattgctgatgggaaccttgtgaaaggacctgcatctcctggacaaaccaagacaccta 825
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                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Human; high bone mass; HBM gene; Zmaxl gene; chromosome 11; 11q13.3; sequence tagged site, STS; osteoporosis; osteopothic; gene therapy; antisense therapy; vaccine; bone disorder; Paget's disease; sclerostosis; osteomalacia; fibrous dysplasia; ds.
                                                                        2 TTTTACCTGATGACCCAGATAAGAAACCACAGGCAAAGCAGTTGCAGACCAAGAAACCAC 61
                                                                                                                                                                      62 AGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAAGAC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 66933 BP; 14237 A; 17817 C; 18323 G; 16556 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New high bone mass (HBM) and Zmaxl genes and proteins useful modulating bone mass for the treatment of e.g. osteoporosis -
                                     Indels
                                   52;
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21.4%; Score 32.8; Dl 55.2%; Pred. No. 2.6; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Human HBM gene region b200e21-h_contig4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GCAAGAAAGAAGTGCAAAGACTTACT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                               ABA82625 standard; DNA; 66933 BP
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                                     64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53; Conservative
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Matches 53; Conserv
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                                     Matches
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The present invention describes the human Zmax1 gene and the high bone mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM genes have osteopathic activities. The genes can be used in gene therapy, and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoporosis, paget's disease, sclerostosis, osteomalacia and fibrous dysplasia. ABA82038 to ABA82700 and AAG68168 to AAG68193 represent sequences used in the exemplification of the present invention.
                                                                                                                                                      Human; high bone mass; HBM gene; Zmaxl gene; chromosome 11; 11q13.3; sequence tagged site; STS; osteoporosis; osteopathic; gene therapy; antisense therapy; vaccine; bone disorder; Paget's disease; sclerostosis; osteomalacia; fibrous dysplasia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New high bone mass (HBM) and Zmaxl genes and proteins useful for modulating bone mass for the treatment of e.g. osteoporosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson ML;
                                                                                                                       Human HBM gene region b527d12-h_contig309G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 51; Page 258-302; 443pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recker RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
                  ABA82623 standard; DNA; 72049 BP.
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05-APR-2000; 2000US-0544398.
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                                                                                      25-JAN-2002 (first entry)
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                                                   ABA82623;
ABA82623
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Query Match
21.3%; Score 32.6; DB 22; Length 72049;
Best Local Similarity 60.9%; Pred. No. 9.5;
Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
Qy 61 CAGGCAAAGCAGTGCAGACCGGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTT 120

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121 GCAAGAAAGAAGTGCAAAGACTTACT 147

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43409 gataaagaaagtctgaaaagacttact 43435

Search completed: August 2, 2002, 20:47:37 Job time: 25948 sec

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	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
OM nucleic - nuclei	nucleic search, using sw model
Run on: Au	August 2, 2002, 16:52:15; Search time 8940.62 Seconds (without alignments) 230.972 Million cell updates/sec
Title: US-(Perfect score: 153 Sequence: 1 A)	US-08-973-363-5 153 1 ATTTACCTGATGACCCAGATGCAAAGACTTACTGGTGCA 153
Scoring table: ID Ga	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched: 13	13736207 segs, 6748477542 residues
Total number of hit	Total number of hits satisfying chosen parameters: 27472414
Minimum DB seq length: 0 Maximum DB seq length: 2	length: 0 length: 2000000000
Post-processing: Minimum Match 0% Maximum Match 10 Listing first 45	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database : ES 1: 2 2: 3 3: 3 4: 5 6: 6 10: 10: 11: 13: 13: 14: 11: 11: 11: 11: 11: 11: 11: 11: 11	EST:* : em_estba:* : em_esthum:* : em_esthum:* : em_estru:* : em_estp:* : em_e

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

BM024825 fu13809.x AL658477 AL658477 AL322865 Terracedon AL322865 Terracedon AL202807 Terracedon AL200707 Terracedon AL200707 Terracedon BM163891 ESF566414 AL332812 Terracedon AL293139 Terracedon AL393139 Terracedon AL393139 Terracedon AL341950 Terracedon AL341951 Terracedon AL341951 Terracedon AL346289 Terracedon AL3463999 Terracedon AL3463999 Terracedon AL356703 Terracedon AL356703 Terracedon AL309319 Terracedon	BB155356 BB15536 BB15
BM024825 BM185005 AL658477 CNS055XR CNS04126 CNS024UQA CNS024UQA CNS024UQA CNS024UQA CNS05AUQA CNS05BSQ CNS05BSQ CNS05SUQA	ALIGNMENTS 1-length enriche a A130024116 3, a (CHD-1) mRNA, 88254 Chordata; Cran i; Rodentia; Sciuu i, P., Fukuda, S. iyama, T., Miyaza i, Saito, R., Sai inagawa, A., Shi A., Saito, R., Sai inagawa, A., Shi A., Saito, R., Sai inagawa, T., et a sequence vers is sequence vers i
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 BBL55356 LOCUS DEFINITION DEFINITION ACCESSION VERYWORDS SOURCE ACTHORS AUTHORS AUTHORS COMMENT COMMENT

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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Multicapillary sequencer. Genome Res. (10, 11), 1757-1771 (2000) Multicapillary sequencer. Genome Res. (2000) Multicapillary Sequencer. Genome Res. (2000) Multicapillary Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. (11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa Hayashizaki, Y.
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 660)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Rawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,K., Sano,H., Sasaki
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
peneare full-length cDNA libraries for rapid discovery of new
agi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/db_xref="taxon:10090"
/clone=1130070B13"
/clone=11b=**TRIKEN full-length enriched, 12 days embryo spinal ganglion"
                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jul 21, 2000 this sequence version replaced gi:9356558.
Contact: Yoshihide Hayashizaki
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/dev_stage="12 days embryo"
/lab_host="DH10B"
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JOURNAL
COMMENT
                                                                                              ORGANISM
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                                  KEYWORDS
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Asshizaki,Y.
RikEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. .. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                             Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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                                                                                                                                                                                                                  Computer-based methods for the mouse full-length cDNA
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ches 20; Indels
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/dev_stage="16 days neonate"
/lab_host="DH10B"
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80.28;
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81; Conservative
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source

FEATURES

Query Match Best Local S

Matches

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BB461065

RESULT

ACCESSION

BASE COUNT

ORIGIN

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Contact: Robert Strausberg, Ph.D.
Email: Gapbs remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
NR Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Nww-bio.llnl.gov/bbrp/image/mage.html
Insert Length: 1924 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 418.
                                                                                                                                                                                                                                                                                                                                           547 bp mRNA linear EST 07-MAR-2000 wm95fil.xl NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443725 3' similar to SW:CHDI_HUMAN 014646 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1; mRNA sequence.
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//do.xref="taxon:9506"
//do.xref="taxon:9506"
//clone=_lib="NCI_CGAP_Ut2"
//clone=lib="NCI_CGAP_Ut2"
//clone=lib="NCI_CGAP_Ut2"
//clone=lib="NCI_CGAP_Ut2"
//clone=lib="NCI_CGAP_Ut2"
//clone=lib="tope" unchors, your vertus, vector: pcMV-spoRT6; Site_l: Sall;
//orte="Organ: uterus, vector: pcMV-spoRT6; Site_l: uterus, vector: pcMV-spoRT6; Site_l: uterus, vector: pcMV-spoRT6; Site_l: uterus, vecto
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 547)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap,
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                   52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
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87.8%; Pred. No. 1.3e-07;
tive 0; Mismatches 10
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Best Local Similarity 87.8'
Matches 72; Conservative
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Unpublished (1997)
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AL601246 430 bp mRNA linear EST 14-AUG-2001 DKFZp313J1040_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone DKFZp313J1040 5', mRNA sequence.
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBP (Mational Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No sI sequence available.
This clone (DKEZPAIJA1040) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
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/db_xref="taxon:0506"
/clone="DrEPp31311040"
/clone_lib="313 (synonym: hlcc2)"
/dev_xape="adult"
/lab host="Dreplos"
/note="yector: pTriplEx2; Site_1: S
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AL601246.1 GI:15164752
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                                                                                                                                                                                             Luckaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (Dasses 1 to 821)
In (Dasses 1 to 821)
In (Datibution: Init) gov.

In Strauber of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: CLONETECH Laboratories, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. k column: 18
http://image.llnl.gov. k column: 18
http://image.llnl.gov. column: 18
http://image.llnl.gov. column: 18
http://organism="Homos sapiens"
//db_xref="taxon:9606"
/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggccgctcggcc): Site_2: Sfil (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGAGGGGCGCATG-G-GT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb): 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Kukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 866)
601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 AAGAAACCACAGGCAAAGCAGTIGCAGACCCGIGCAGATTACCTCATTAAATTACTGAAT 111
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Pred. No. 1.4e-07;
0; Mismatches 10; Indels
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149 c 190 g 137 t
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AU125712.1 GI:10950428
                                                                                      BF239967.1 GI:11153890
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Best Local Similarity 87.8
Matches 72; Conservative
                           mRNA sequence.
BF239967
                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                      AUTHORS
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SOURCE
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Salto, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S., Isogai, T.)

Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'-6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó;
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                                                                               HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Chases 1 to 1028)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DTIP/DIP
Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9753 row: h column: 16
High quality sequence stop: 488.
Location/Qualifiers
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87.8%; Pred. No. 1.4e-07;
ive 0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .866
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4002061"
/clone_lib="NT2RM4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 AAAGACCTTGCAAGAAAGAAG 133
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BE895133.1 GI:10358221
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Best Local Similarity 87.0.
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                                                       Isogai, T.
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Mon Aug

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BB834922 BE84922 RIKEN full-length enriched, mammary gland RCB-0527 BB84922 RIKEN full musculus eDNA clone G930033721 3', mRNA MRNA CLONE G930033721 3', mRNA
                                                                                                                                                                                                                                                                                         AL644594 XGC-egg Silurana tropicalis CDNA clone LIBIdl2 5', mRNA
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Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea, Pipidae;

Xenopodinae; Silurana.

1 (Dases I to 643)

Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.

Sangar Xenopus tropicalis EST project 2001 (10_2001)

Contact; Huckle E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="Escherichia coli XLI-blue"
//lab_host="Escherichia coli XLI-blue"
//note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
ECORI at the 5' end and NotI at the 3' end"
125 c 156 g 141 t 1 others
                                             52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
                 52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hinton, Cambridgeshire, CB10 1SA, UK
Email: tropésanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_ESTORONE_ID: LIEIG12.pic
Sequencing primer: PIC
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                            265 AAAGATCTGCTTAGGAAAGAAGCACAAAGACTTTCTAGTGGA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Silurana tropicalis"
/db_xref="texon:8364"
/clone="LiBidis"
/clone_lib="x6C-egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
BB834922
BB834922.1 GI:17013165
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AL644594.1 GI:16796719
                                                                                                                                                                                                                                                                                                                                                                                                                                           western clawed frog
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BB834922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
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VERSION
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                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL659353 XGC-neurula Silurana tropicalis cDNA clone TNeu045e20 5',
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                        /clone_lib="NIH_MGC_72"
/tisbase_type="mealanotic" melanoma"
/tab_host="hild (phage=resistant);
/note="norgan skin; Vector: pCMV-SPORT6; Site_1: Not1;
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/note_2: Salı; Cloned unidirectionally. Primer: Oligo dT.
/note_2: Salic isec 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="neurula"
//ab_host="seperichta coll DH10B"
//ab_host="seperichta coll DH10B"
//ab_host="seperichta coll DH10B"
//ab_host="seperichta"
//acce="vector: pCS107; Site_1: EcoRI: Site_2: NotI: cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut CDNA was then ligated into pCS107 with a last the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanger Xenopus tropicalis EST project 2001
TROPICALS_SEQUENCE_ID: TNeu045e20.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                *Match 43.1%; Score 66; DB 10; Length 1028; Local Similarity 87.8%; Pred. No. 1.4e-07; Local Similarity 0; Mismatches 10; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Silurana tropicalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cambridgeshire, CB10 1SA, UK
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/clone="TNeu045e20"
/clone_lib="xGC-neurula"
                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                 /clone="IMAGE:3921087"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 AAAGACCTTGCAAGAAAGAAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: trop@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL659353.1 GI:17672995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Silurana.
1 (bases 1 to 593)
                                                                                                                                                                                                                                           Technologies.'
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Silurana tropicalis
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Matches 78; Conservative
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AL659353
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Best Local 5
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source
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ORIGIN
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AL659353/c
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JOURNAL
COMMENT
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EST 05-JUN-2000

ORGANISM

KEYWORDS

SOURCE

REFERENCE AUTHORS JOURNAL COMMENT

TITLE

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/organism="Homo sapiens"
/db_xref="taxon:9666"
/db_xref="taxon:9666"
/clone_lib="BN0047"
/dev_stage="Addult"
/note="Organ: breast_normal; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
is a 154 c 126 g 241 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-QV3-BNO047-150 Seq primer: puc 18 forward High quality sequence start: 19 High quality sequence start: 19 High quality sequence store; 578.
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotz, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases I to 686)

1 blass Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB830730 RIKEN full-length enriched, mammary gland RCB-0527 J9-NOV-2001 J9-NOV
                    AW997058 686 bp mRNA linear EST 05-JUN-200 QV3-BN0047-150400-152-c03 BN0047 Homo sapiens cDNA, mRNA sequence. AW997058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 AGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAATA 112
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Pred. No. 7.6e-06;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
                                                                                                                                                                                                   AW997058.1 GI:8257292
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Fax: +55-11-2707001
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Matches 66; Conservative
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AW997058/C
                                                                                               DEFINITION
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                                                                                     SM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E (Dases 1 to 446)

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,

Hayatau,N., Hiranoto,K., Hiraoka,T., Imorane,T., Imorane,T., Imorane,M., Nojina,Y., Konno,H., Kouda,M., Matsuyama,T.,

Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,T., Okido,T.,

Salto,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,

Shibata,K., Shinaya,T., Sogabe,T., Suzuki,H., Tagawa,A., Shiraki,T., Sogabe,T., Suzuki,H., Tagawa,A., Watahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,

Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
Fax: 81-45-503-9228
Fax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (12), Sugahara, Y. and Haysahizaki, Y. and Haysahizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Pred. No. 1e-06;
0; Mismatches 24; Indels
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99 c 108 g 100 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="G930033J21"
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76.28;
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Gaps

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BASE COUNT ORIGIN

FEATURES

Matches

à qq δ RESULT 11

EST 05-JUN-2000

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UNSU4DVG 856 bp DNA linear GSS 21-MAY-2000 Tetracdon nigroviridis genome survey sequence T7 end of clone 103KO8 of library G from Tetracdon nigroviridis, genomic survey sequence.
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Final: asimpson.out.g.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-230

200-102-d03&st3=2000-02-38&t-1)

Seq primer: put 18 forward

High quality sequence start: 2

High quality sequence start: 2

High quality sequence start: 2

High quality sequence start: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Language, and Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                  AW996787 11near EST 05-JUN-200
QV3-BN0047-230200-102-d03 BN0047 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 337)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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/db_xref="taxon:9606"
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/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hiraoka, T., Hiraoka, T., Mocane, T., Inotani, K., Ishii
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Konoda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Soaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagawa
A., Takahashi, F., Takaku, Akahira, S., Tamaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Sciences Center(GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 438)
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/clone=1kb=RrkKR full-length enriched, mammary gland
RCB-0527 Jyg-WC(B) cDAR"
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/cell_line=RCB-0527 Jyg-WC(B)"
/cell_line=RCB-0527 Jyg-WC(B)"
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Location/Qualifiers
    BB830730.1 GI:17008973
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Hayashizaki,Y.
                                                                                       house mouse.
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 512)
1 (bases 1 to 512)
1 (clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
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                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence Unpublished
                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 856)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                        retraodontidae; Tetraodon.
1 (bases 1 to 856)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
                                                                                                                                                                                                                                                                       Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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/clone_lib="G"
/note="Genoscope sequence ID : COBG103BF04LP1~end : T7"
308 c 252 g 206 t 6 others
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/clone="103K08"
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                                           GSS; genome survey sequence. Tetraodon nigroviridis.
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                                                                                      Tetraodon nigroviridis
                      AL286261.1 GI:8024707
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ilarity 67.3%;
Conservative
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Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Rohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Washu Zebrafish EST Project 1998

Unpublished (1998)

Other ESTS: fq17e65.y1

Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University Good
Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: John Ngal. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Mashington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@tesgen.com) and
RessourcenzentrumPrimarDatenbank, Berlin, Germany (web address:
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/lab_host="E. coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www.rzpd.de)
Trace considered overall poor quality
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High quality sequence stop: 1.
Location/Qualifiers
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Run on:

Result

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Query Best] Match	/ Match Local Similarity 100.0%; Pred. No. 0; nes 660%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	GAAGGCCTGG
QQ	
y d	61 CCGCCGAGCCGGACGCAGGTATTGGGCAAAAATCTTGGCCATCTGTAGAGAATAG 120
Qy 1	1 CAAGTCAAACGCATTACTTCGAAAACATACGGAGTACCAGAAAGGGGGATTCTTGACCTAC 18
Db 1	
0y 1	181 ACCTIGIAACCIGAGIGGACITICTITITAACTICTIAATACTIACAATGAATGGGCACA 240
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Oy 2	241 GTGATGAAGAAAGTGTAAGAAACAGCAGTGGAGAGTCAAGCAGATCAGATGATGATTGT 300 241 GTGATGAAGAAAGTGTAAGAACAGTAGAAGAGTGAAGAGTAAAACAATGAAGAATGATGAATGA
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Db 3	
	GCCAGTCAGGTAGCAGTGACTCTGAATCTGGTTCAGAGTCAGGCAGTCAATCCGAATCAG 4
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Qy 4	21 AGICTGACACATCTAGAGAGAAACAAGTTCAAGCTAAACCTCCGAAAGCTGACGGAT 480
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Qy 4	81 CTGAGTTTTGGAAGTCCAGTCCAAGCATACTTGCTGTACAGAGATCAGCAGTGCTCAAGA 540 [
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9 KO	601 GTAGTGAAGATTCTGCCGATGATTCGTCCAGTGAAACTAAGAAGAAAAAAGCATAAAGGTG 660
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_	51 AAGACTGGCAAATGTCAGGGTCAGGGTCAGTATCAGGAACTGGTTCTGATTCTGAATCGG 72
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-	01 ATAAGAGAGATCTCGTCGCCAGGCAACAGGAATCTTACTTA
6 qa	01 ATAAGAGAGTCTCGTCGCCAGGCAACAGTGAATGTTAGTTA
	61 CCAAGACAGATICTGATGATTTGCTGGAAGTTTGTGGAGGAGGATGTCCCACAGACTGAAG 102
6 qa	61 CCAAGACAGATTCTGATGATTTGCTGGAAGTTTGTGGAGAGGATGTCCCACAGACT

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Οy	5461	AAAGATATGGACTGGATATTCTATCAGTAGCAGTATTGTTACTTCTTCCAGGA 55	
Dp	5461	CTTGAAAGATATGGACTGGATATTCTATCAGTAGCAGTATTGTTACTTTCCAGGA 55	~
oy G	5521	TGCAAGGTCTATTATCCCAACAGAAAAAAATATTTTGTATTAAAGTTTATGCTGCAC 558	280
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δy	5641	CCTCAACACTGCCCCTTTCAGACTGGATCTTACTATAAAACTCTTCATGTCAAAGTGG 57	00
qq	5641	ACCICAACACTGCCCCTTTCAGACTGGATCTTACTATAAAACTCTTCATGTCAAAGTGG 57	00,
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δý	5761	TTGTTTTATTTCTTGGTAGAGAACTCTC 58	320
QQ	5761	TATGTTTCAGGAAAGAATGGGGGGATTTATTTTGTTTATTTCTTGGTAGAAACTCTC 58	320
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δy	6001	AAAAAAAAACACAACAAAACCAACAAATGGCTGTAAATTATTGTAAATTAATT	090
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δδ	6061	TITITCCGTCAGGCTTTTTTGGCTGTTCCTTTCCCCAACACTCAGGCCT 61	.20
qq	6061	TGAGCTTTTTTCCGTCAGGCTTTTTTGGCTGTTCCTTTCCCCAACACTCAGGCCT 61	.20
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Οy	6361	CATTGGTTTAAAAGAAGGAAGTGTTCTATAGGTGAACACTTCAAAACCCAGATCA 64	120
qq	6361	GTGCATTGCTTTAAAAGAAGGAAGTGTTCTATAGGTGAACACTTCAAAACCCAGATCA 64	C)
QY	6421	GCCAAGATTCATTGTAAATCCATTTGTTTTCCCTCTTTAACATGGGCAATAATGTCAAAAT 648	081
qq	6421	CCAAGATTCATTGTAAATCCATTTGTTTTCCCTCTTTAACATGGGCAATAATGTCAAAT 64	081

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Gaps

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in 1223 c 1520 g 1683 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GTGATGAAGAAAGTGTAAGAAACAGCAGTGGAGAGTCAAGCAGATCAGATGATGATTCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GGTCAGCTTCAGGTTCTGGATCTGGTTCAAGCTCTGGAAGCAGTAGCGATGGAAGTAGCA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.9%; Score 6334; DB 5; Length 6872; 96.2%; Pred. No. 0; tive 0; Mismatches 0; Indels 264;
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Best Local Similarity
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FLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVTKGS
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LFKEPEGEEQEPQEMOIDEILKRAETERBEGELTYGGFKVANFSNMDEDIE
LEPERNSRWHEEI IPESQRRIEBEERQKELEEIYMLPRMRVGAQISFNGSBGRRSR
SRRYSGSDSDSTTERKREKKRGRPTIPRENIKGFSDAEIRRTKSYKKFGGPLERLD
AVARDAELVDKSETDLRRLGELVHNGCIKALKDNSSGQERAGGRLGKVKGPTFRISGV
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STSGFLNIMMELKKCCNHCYLIKPPDDNEFYNKQEALQHLIRSSGKLILLDKLLIRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A CHD1 gene is 2 chromosome linked in the chicken Gallus domesticus Gene 197 (1-2), 225-229 (1997)
97473516
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Griffiths, R. and Korn, R.M.
Direct Submission
Submitteed (16-MAY-1997) Zoology, Molecular Lab, Glasgow University,
Glasgow G12 800, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 6872)
Griffiths, R. and Korn, R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF004397 6872 bp mRNA linear VRT 08-OCT-19 Gallus gallus chromo-helicase-DNA-binding on the Z chromosome protein, variant with hydrophilic domain, (CHD-2) mRNA, complete
                                6481 GIGCIAIGCAGCAGTIAAIAITITAGAAGAITITGAAIGACITITATIAACAGAATIGITAC 6540
                                                                                                                    6541 AATGCACACTGATTGTACATAGATAACTTCTATCTGACAAATTAAATTAAACTTAAAACGAA 6600
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/gene="CHD-z"
/function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
/codon_start=1
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/db_xref="taxon:9031"
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228. .5654
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KEYWORDS
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4-4 0-0 4-4	CCAAGACAGATTCTGATGATTTGCTGGAAGTTTGTGGAGAGGATGTCCCAC	CTGGTGCCTCAACCACCATCTATGCCGTTGAGGCAGATGGTGACCCAAATGCTGGGTTTG [TCCATAACACTTGGGAAACTGAAGAAACGCTGAAGCAACAAAATGTTAAAGGAATGAACA	CAGAAGATGTGGAATATTATAACTGCCAGCAGGAGCTTACAGATGATCTGCACAAATATTIIIIIIIIII	ACTACTATTGCAAATGGCAGGGTCTGCCTTACTCAGAATGTAGCTGGGAAGATGTGCTCC	CTACTCCCTTTAAGGACTGCAAGGTTCTAAAACAGAGACCAAGATTGTTGCACTGAAGA	GATTGAATTGGCTCGCTCATTCATGGTGCAAAGGAAATAGTTGTATTCTTGCAGATGA 	AACIGIATGGCCCTTTTCTTCTGCGCGTGCCACTTTCTACCTTGACATCTTGGCAAAGAG
781 781 841 901	9 9 7 7	1081 1081 1141 1141	1201 1201 1261 1261	1321 1321 1381 1381	1441 1441 1501 1501	1561 1561 1621 1621	1681 1681 1741 1741 1801	1801
Qy Qy Qy	oy oy	oy Oy Oy	03 04 05	Qy Db Db	oy Oy Ob	oy Oy Ob	Qy Qy Qy	qq

2040 2040 2100 2100 2160 2220 2220 2280 2280 2340 2340 2400 2400 2460 2460 2640 2640 2700 2700 2760 2760 2820 2820 2940 2940 AGATTCAAACTTGGGCTCCTCAGATGATGCTGTAGTTTACTTAGGAGATATAACTAGTA GATTAGGTATTAACTTGGCATCTGCTGACACTGTAGTTATTTTGATTCTGACTGGAATC 2941 ATATTTATCGGCTAGTCACAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAAGA AAGAGCTTGAACCATTTTTACTAAGAAGAGTTAAAAAAGATGTAGAAAAGTCTTTACCTG GGATTTTAACAAGGAATTATAAAGCCCTCAGTAAAGGTTCAAAAGGCAGTACCTCAGGCT GGGCATTCATAGGAGTTGATGAAGCTCATCGTTTAAAAAAATGATGACTCTTCTGTACA GGGAAGATTTTGAAGAGGAGCATGGCAAAGGAAGAGAGTATGGTTATGCAAGTCTTCACA CTAAGGTTGAACAAATTCTGAGGATGGAAATGAGTGCATTGCAGAAGCAATATTACAAGT GGATTTTAACAAGGAATTATAAAGCCCTCAGTAAAGGTTCAAAAGGCAGTACCTCAGGCT TTCTGAACATTATGATGGAACTTAAGAAGTGTTGTAACCATTGCTACCTCATTAAGCCAC CAGATGATAATGAATTCTATAATAAACAGGAGGCCTTACAGCATTTGATACGTAGCAGCG GGAAACTAATCCTTGACAAGCTACTGATTCGTCTGCGAGAACGTGGCAACAGAGTTC TGATTTTCTCTCAGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTATCGCC GATTAGGTATTAACTTGGCATCTGCTGACACTGTAGTTATTTTGATTCTGACTGGAATC CACAGAATGATCTGCAGGCGCGAGGGCGGGGGCTCATAGAATTGGACAGAAGAAGAAGGTTA GAAATATGATAAGGACTCATGAATGGATGCATCCACAGACTAAAAGGTTTAACA ATTCCCTCAAAGAGCTGTGGTCTTTGTTGCATTTCATCATGCCAGAAAATTTTCCTCCT 1981 2041 2161 2461 2521 2581 1861 1861 1921 1921 1981 2041 2101 2101 2161 2221 2221 2281 2281 2341 2341 2401 2401 2461 2521 2581 2641 2641 2701 2701 2761 2761 2821 2821 2881 2881 g 원 qq QQ g QQ ŏ Op g g g Op g qq g g qq g Ω δ ŏ δ οy δ ٥y δý QY ŏλ Ω òγ δ qq ŏ δ δ δ

DD ATGGCTATGGCAGCTGGGAAATGATAAAATGGATCCAGATCTCAGCTTAACACAGAAGA 4080	QY 4261 TAAAAGAATAAAAGAGTGATTCTTCACCACAACCCTCAGAAAAATCTGATGAAGATG 4320 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 4338	QY 4338	4350 TABAAGAATCCACACAGAAAGAAAAGAGGAAGGAAGGAAGGAA	QY 4417 CAACCAGTGAACCAGTTCCTATCTCAGAAGAATCTGAAGAACTCCATCAGAAGACATTTA 4476 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	4537 AGAAGGGCCTTTCTGAAAGGAGCAGCTGGAACATACTAGGCAGTGTCTAATCAAAATTG	OY 499/ GGGATCACATTACAGATUCCTGAGAGGAGTACACAGATUCCGAGGAGGAGGAGA 4656	4717 AACTCTACAAACATGCAATCAAAAAGCGCCAAGAGTCTCAGCAACACAATGACCAAAACA [Oy 4837 CTACAAACCATGATGGTAGCAGGGACAGTTATTCTTCTGATAGACATTTATCACAAT 4896
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	3181 AGGAAATGGATATAGATGAAATCTTGAAGAGGCTGAAACTCGGGAAATGACCGGCTCAACTCGGGAAATGACCAGGTC	ACTITICCAAIATGG TGGGAAGAATCATCC HHIHHHHHHH TGGGAAGAATCATCC SAACTTGAAGAATAT	3421 ACATGCTCCCGAGGATGAGAAACTGTGCAAAACGGATCAGCTTT 3421 ACATGCTCCCGAGGATGAGAAACTGTGCAAAACAGATCAGCTTT 3421 ACATGCTCCCGAGGATGAGAAACTGTGCAAAACAGATCAGCTTT	QY 3481 GACGCAGTAGGACCAGAAGATTTTGGGATCTGATAGTGACCATCACAGAAAGAA	3601 ATGCAGAGATCAGGCGGTTTATCAAGAGATTACAAGAAATTTGGTGGCCCTCTGGAAAGGT	DD 3001 TAGATGCTGTAGCTGAACTGGTGATGTTGATAAATCTGGACAGACCTTAGACGTT 3720 QY 3721 TGGGTGAACTTGTACATAATGGATGATTAAAGGTTTAAAGGACAATTCATCTGGACAAG 3780 DD 3721 TGGGTGAACTTGTACATAATGGATGAATTAAAGGTTTAAAGGACAATTCATCTGGACAAG 3780 DD 3721 TGGGTGAACTTGTACATAATGGATGCATTAAAGGACAATTCATCTGGACAAG 3780	OY 3781 AAAGAGGAGGAGTAGACTTGGGAAAGTTAAAGGCCCAACGTTTCGAATCTCAGGAGTGC 3840	TTCCTTCACATCCAGAAGAAAGGAAAGATATGTCATCCCATGCCACCCAGGCTGCTC [Oy 4021 AIGGCTATGGCAGCTGGGAAATGATAAAATGGATCCAGATCTCAGCTTAACACAGAAGA 4080

Qy Db	4897	ACCATGATCATCACAAAGACAGGCATCAGGGAGATGCTTACAAGAAAGTGACTCCAGGA 4956 	
QY	4957 5221	AAAGGCCATATICAGCCTTCAGTAATGGAAAAGATCACAGAGACTGGGATCACTACAAAC 5016 	
Q7 Db	5017	AGGACAGCAGATACTACAGTGATAGTAAACATAGAAGTTAGATGACCACAGGAGCAGAG 5076 	
oy Og	5077	ACCACAGGTCAAACCTGGAAGGAAACTTAAAAGACGGGGGTCATTCAGATCACCGCT 5136 	
Oy Db	5137	CCCATTCAGACCACAGGATACACTCAGATCACCGTTCCACTTCAGAATACAGCCATCATA 5196 	
Qy	5197 5461	AATCTICGAGAGATTATAGATACCACTCAGACTGGCAAATGGACCACAGAGCTTCTGGTA 5256 	
Qy	5257 5521	GTGGCCCGAGGTCACCACTAGATCAGAGGTCTCCTTATGGTTCAAGATCTCCCCTAGGAC 5316 	
Qy Db	5317	ACAGATCTCCATTTGAACACTCATCAGATCACAAAGTACACCTGAACATACAT	
QY Dp	5377	GCCGGAAGACATAACAAAGACTGACATTTCTGGACCTTCTTTTAGCCATATACAGTAA 5436 	
Qy Dp	5437 5701	ACTAACACAGTAATTGCCTTACATGACTTGAAGATATGGACTGGATATTCTATCAGTAG 5496 	
Qy	5497 5761	CAGTATIGTTACTTCCTTCCAGGATGCAAGGTCTATTATCCCAACAGAAAAATATT 5556 	
Qy Dp	5557 5821	TIGIATITAAAGTITAIGCIGCACIGIGCIGCAAAIGIIGIGGCACITITITITAAGAA 5616 	
Qy Dp	5617 5881	ATGGAAGATGTTTACTTTTACAGGGACCTCAACACTGCCCCTTTCAGACTGGATCTTACT 5676 	
QY Db	5677	ATAAAACTCTTCATGTCAAAGTGGTTCTAGGCTGAACACAGATTAAATTATGTTTGTAAA 5736 	
OY Db	5737 6001	TGAACACTTAAACACTGACCTGTGCTTATGTTTCAGGAAAAGAATGGGGGATTTATTT	
Oy Db	5797 6061	TITATITCIIGGIAGAGAACTCICAAGGACTIIGIICACITICCAAAGCIACIIGIIIAC 5856 	
Qy Db	5857 6121	ATTGTACACTGCGACCTTGCCGCTTTTCATCACAAGCTTGAATATTTAAATTCTGTA 5916 	
oy Dp	5917 6181	CCTACAGTTGTAAAATAGCCAGGATTTCTCCTGTTTGTGATCAGTTATAATGCCTTTTTA 5976 	

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                                                                                               GCTGTAAATTATTGTAAATTAAATGAGCTTTTTTCCGTCAGGCTTTTTTTGGCTGT
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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                        602 TAGTGAAGATTCTGCCGATGATTCGTCCAGTGAAACTAAGAAGAAAAAGCATAAAGATGA
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/db_xref="G1:2645429"
                                            164. .5293
/gene="CHD1"
/codon_start=1
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6 G	62,	TGGTTTAAATTGGCTTGCTCATTCTTGGTGCAAAGGAAATGGTTGTTGTTGTTGTGTGTG	
Qy Db	1739	AATGGGTCTGGGTAAAACAATACAAACAATTTCTTTTCT	
Qy Dp	1799	TCAACTGTATGGCCCTTTTCTTCTGCGCGTGCCACTTTCTACCTTGACATCTTGGCAAAG 1858 	
Oy Db	1859	SCTGTAGTTTACTTAGGAGATATAACTAG 1911 	
Qy Db	1919	TAGAAATATGATAAGGACTCATGAATGGATGCACACAGACTAAAAGGATTAAA 1978 	
λ O P	1979	CATACTTCTGACGACATATGAAATTTTACTGAAGGATAAGTCATTCCTTGGTGGTCTCAA 2038 	
Q.Y	2039	TTGGGCATTCATAGGAGTTGATGAAGCTCATCGTTTAAAAAATGATGACTCTCTTCTGTA 2098 	
Qy Dp	2099	CAGGACTTTAATAGACTTTAAGTCCAACGACTTCTGATTACTGGAACCCCACTGCA 2158 	
Oy Db	2159	AAATTCCCTCAAAGAGCTGTGTGTTTTGTTGCATTTCATCATGCCAGAAAATTTTCCTC 2218 	
λά	2219	CTGGGAAGATTTGAAGAGGAGCATGGCAAAGGAAGAGTATGGTTATGCAAGTCTTCA 2278 	
Qy Db	2279	CAAAGGGCTTGAACCATTTTTACTAAGAAGAGTTAAAAAGATGTAGAAAAGTCTTTACC 2338 	
Qy Dp	2339	TGCTAAGGTTGAACAAATTCTGAGGATGGAAATGAGTGCATTGCAGAAGCAATATTACAA 2398 	
Qy Db	2399	GTGGATTTTAACAAGGAATTATAAAGCCCTCAGTAAAGGTTCAAAAGGCAGTACCTCAGG 2458 	
Qy	2459	CTTTCTGAACATTATGATGGAACTTAAGAAGTGTTGTAACCATTGCTACCTCATTAAGCC 2518 	
Qy	2519 2464	ACCAGATGATAATGAATTCTATAATAAACAGGAGGCCTTACAGCATTTGATACGTAGCAG 2578 	
Qy Dp	2579	CGGGAAACTAATCCTTCTGACAAGCTACTGATTCGTCTGCGAGAACGTGGCAACAGAGT 2638 	
Oy Dp	2639	TCTGATTITCTCTGAGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTATCG 2698 	
Oy Db	2699	CCAGITICCCITCCAGAGACITGAIGGAICAATAAAAGGGGAAIIGAGGAAGCAAGCACCT 2758 	
λά	2759	GATCATTTCAATGCAGAAGGATCAGAGGATTTCTGTTTTTTACTGTCTACAAGAGCTGG 281	

3178 3538 3719 TITGGGTGAACTTGTACATAATGGATGCATTAAGGCTTTAAAGGACAATTCATCTGGACA 3778 2763 2824 TCCACAGAATGATCTTCAGGCACAGGCTAGAGCCCATCGAATTGGCCAAAAGAAAACGGT **AGGATTAGGTATTAACTTGGCATCTGCTGACACTGTAGTTATTTTTGATTCTGACTGGAA** AGGICTAGGGATTAATTTAGCCTCTGCTGACACTGTTGTTATTTTGATTCCGATTGGAA TAATATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAA 3119 TATTTTGAAGTTTGGTGCTGAGGAACTCTTTAAAGAACCTGAAGGAGAAGAACAGGAGCC 3839 GCAGGTGAATGCAAAACTAGTCATCTCTCACGAAGAGGGGGCGCCCACCACTGCACAAATC TCCACAGAATGATCTGCAGGCACAGGCGAGAGCTCATAGAATTGGACAGAAAACAGGT GAAGAAGATGGTGCTAGACCATTTAGTAATTCAGAGAATGGACACGACAGGAAAAACTGT TCTGCATACAGGTTCAACTCCATCAAGCTCTACACCTTTTAATAAAGAAGAGTTATCAGC GGATGAAGATGATTGAGTTGGAACCAGAAAGAAATTCAAGAAATTGGGAAGAAATCAT ATACATGCTCCCGAGGATGAGAAACTGTGCAAAACAGATCAGCTTTAATGGGAGTGAAGG 3599 TGATGCAGAGATCAGGCGGTTTATCAAGAGTTACAAGAAATTTGGTGGCCCTCTGGAAAG ACTGGGAGAATTGGTACATAATGGTTGCATTAAAGCATTAAAAGGATAGTTCTTCAGGAAC AGAAAGAGCAGGAGGTAGACTTGGGAAAGTTAAAAGGCCCCAACGTTTCGAATCTCAGGAGT 2939 2999 2944 3419 2704 3059 3004 3299 3664 2819 2764 2879 3479 3659 3779 3724 δy g δ Dp òγ g Qγ qq Óγ g οy g õ Db Qγ qq ŏ q à g οy g Qγ g δy g δ g δ QQ δ g δy g οy

qq	3784	ACAGGTGAATGCCAAACTAGTCATCTCCCATGAAGAAGAATTAATACCTTTGCACAAATC 3843	
γς 10	3899	CATTCCTTCAGATCCAGAAGGAAAGGATATGTCATCCCATGCCACACCAAGGCTGC 3958	
δο <i>ξ</i>	3959	TCACTTCGATAIAGATTGGGGTAAAGAAGATGATTCCAATCTGTTAGTAGGCATCTATGA 40	
3 & 2	01	TATITICALATEGACACTGGGGCAAAASAAATGTAAATTGTTAATTGCGCATCTATA 398 ATATGGCTATGGCAGCTGGGAAATGATAAAAATGGATCCAGATCTCAGCTTAACACAGAA 4071 ATATGCATATGGAAGTGCAAATGATAAAAATGAACAAGAAAAAAAA	
oy ob	07	GATITIACCIGAIGACCCGACAAGAACCCCAGGCAAACACTACAGACCCGTGCAGA 413	
oy og	4139	CTACCTCATTAAATTACTGAATAAGACCTTGCAAGAAAGGAAGCACAAAGGCTTGCTGG 419	
oy Og	4199		
Oy Dp	4256	AAAAATAAAAGAAGAAATAAAGAGTGATTCTTCACCACAACCCTCAGAAAAATCTGATGA 4315 	
Oy Op	4316	AGATGATGAGGAGGAGGATAACAAGGAAATGAAATGAAA	
Qy Dp	4376		
Oy Dp	4436		
Oy Dp	4496	GAGGCCTGICAAAGCAGCACTGAAACAGCTGGATAGACCAGAGAGAGGCCTITCTGAAAG 4555 	
Qy Db	4556 4486	GGAGCAGCAGCAACATACTAGGCAGTGTCTAATCAAAATTGGGGATCACATACAGAATG 4615 	
Oy Db	4616	CCTGAAGGAGTACACAAATCCCGAGCAAATAAAACAGTGGAGGAAAAATTTGTGGATTT 4675 	
Oy Dp	4676	TGTGTCCAAGTTTACAGAATTTGATGCCAGAAAGCTGCACAAACTCTACAAACATGCAAT 4735 	
OY Dp	4736	CAAAAAGCGCCAAGAGTCTCAGCAACACAAAGCCAAAACATTAGCAGCAATGTGAATAC 4795 	
Oy Op	4796	ACATGTAATCAGAANTCCAGATGTGGAAAGACTGAAGGAGACTACAAACCATGATGATAG 4855 	
Oy Dp	4856	TAGCAGGACAGTIATTCTTCTGATAGACATTTATCACAATACCATGATCATCACAAAGA 4915 	
Oy Dp	4916		

4959 5092 5019 5212 5196 5332 5235 5392 5295 5446 5355 5506 5414 5565 5474 5614 5534 5591 5734 5794 5706 5760 5876 5035 5093 GGAAGGAAACTTAAAAAGACAGCCGGGGTCATTCAGATCACCGCTCCCATTCAGACCACAG 5152 5213 TAGATACCACTCAGACTGGCAAATGGACCACAGAGCTTCTGGTAGTGGCCCGAGGTCACC 5272 5615 AAATGGAAGATGTTTACTTTTACAGGGACCTCAACACTGCCCCTTTCAGACTGGATCTTA 5674 5795 GITITATITCTIGGTAGAACTCTCAAGGACTTTGTTCACTTTCCAAAGCTACTTGTT 5854 ACATTGTACACTGCGACCACCTTGCCGCTTTTCATCACAAGCTTGAATATTTAAATTCTG 5914 5020 GGAAGGAAGTTTAAAAGATA---GATCTCATTCTGATCATCGTTCTCACTCAGATCATCG 5535 AAATGGAAAATGTTTACTATTACAGGGACCTCAACACTG-CCCTCCCATACAGGCTGG---GATACACTCAGATCACCGTTCCACTTCAGAATACAGCCATCATAAATCTTCGAGAGATTA 5236 ACATTCAGTTGAACACAAAAGTACACGGAGCATACCTGGAGTAGTCGGAAAAACATAACA 4976 CAGTAATGGAAAAGATCACAGAGACTGGGATCACTACAAACAGGACAGCAGATACTACAG 5036 TGATAG---TAAACATAGAAAGTTAGATGACCACAGGAGCAGAGACCACAGGTCAAACCT 5273 ACTAGATCAGAGGTCTCCTTATGGTTCAAGATCTCCCCTAGGACACAGATCTCCATTTGA 5333 ACACTCATCAGATCACAAAAGTACACCTGAACATACATGGAGTAGCCGGAAGACATAACA 5393 AAGACTGACA----TITTCTGGACCTTCTTTTAGCCATATACAGTAAACTAACACAG TAATTGCCTTACATGACTTGAAAGATATGGACTGGATATTCTATCAGTAGCAGTATTGTT 5566 AAGTTTATGCTGCACTGTGCTGCAAA-----TGTTGTGGCACTTTTTTTAAG 5675 CTATAAAACTCTTCATGTCAAAGTGGTTCTAGGCTGAACACAGATTAAATTATGTTA TACCTACAGTTGTAAAATAGCCAGGATTTCTCCTGTTTGTGATCAGTTATAATGCCTTTT TATGAAACAAA 5985 5855 5761 5915 5447 5153 Ωp g S QQ οy g δ Op Qy Db ò Op οy δŏ g δy QQ οy οy

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DCRVGRRGATGATTITAVEDAGDPAGFERNKEPORDSKENGKRILGGKRROOLDSSEED

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DAJARDAELUKKSETDLRRUGELVHUKGVKALKOSSSGTERAGGKLGKWKGPFFRISG
VOUNAKLVIAHEDELIPLHKS IPSDPERROYTIPCHTKAAHEDIDMGKEDDSNLLIG
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DRSKKSVVSDAPVHTRAKSPENTAKKSENSDENDENIKDSPESK
GLSBERGLEHTRQCLIKIGDHITECLKEYSNPEQIKOWRKNLMIFVSKFTEFDARKLH
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QYHDHHXDRHQGDSYKKSDSRKRPYSSFSNGKDHREWDHYRQDSRYYSDREKHRKLDD
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HRAASSGPRSPLDQRSPYSDAGHRSTPEHTWSSRKT"
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SQSGSSDSDSGSDSGSDSGSSESESDTSRENKVQAKPPKVDGAEFWKSSPSILAVQRSAML
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Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center,
7701 Burholme Avenue, Philadelphia, PA 19111, USA
On Feb 16, 1994 this sequence version replaced gi:293322.
                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus I (bases 1 to 5349)
Delmas, V., Stokes, D.G. and Perry, R.P. A mammalian DNA-binding protein that contains a chromodomain and SNF2/SWI2-like helicase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993) 93211972
                                                                                    MUSCHDIX 5349 bp mRNA linear F
Mouse DNA-binding protein (CHD-1) mRNA, complete cds.
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/protein_id="AAB08486.1"
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/cell_type="plasmacytoma"
1. 5349
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171. .5306
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/gene="CHD-1"
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L10410.1 GI:455014
DNA binding protein.
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Mus musculus
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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MEDLINE
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AUTHORS
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                             RESULT
                                                                                       LOCUS
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DB 10; Length 5349;

Score 3398.2; Pred. No. 0;

51.48; 79.68;

Query Match Best Local Similarity

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1098 GAGCCAGGAGACATACAGTATTAATTAAGTGGAAAGGATGGTCGCACATCCACAACAA 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       978 GAGACAATAGAGGGTTATGGATTGCAGAGTGGGGCGGAAAGGAGCTACTGGTGCTACT 1037
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TTTCTTTTTAACTTCTTAATACTTACAATGAATGGCACAGTGATGAAGAAAGTGTAAGA 260
                    AACAGCAGTGGAGAGTCAAGCAGATCAGATGATTCTGGGTCAGCTTCAGGTTCTGGA
                                                                                                                                                                                      264 TCTGGCTCGAGTTCTGGCAGCAGCAGTGACGGAAGCAGCAGCCAATCCGGGAGCAGCGAC
                                                                                                                                                                                                                                                                                                                                                                                 501 CCAAGCATACTTGCTGTACAGAGATCAGCAGTGCTCAAGAAGCAAC-----AGCAA
                                                                                                                                                                                                                                                                                                                                                                                                         612 TCTGCCGATGATTCGTCCAGTGAAACTAAGAAGAAAAAGGATAAAGATGAAGACTGGCAA
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                                                                                                                                                    TCTGGTTCAAGCTCTGGAAGCAGTAGCGATGGAAGTAGCAGCCAGTCAGGTAGCAGTGAC
                                                                                                                                                                                                                               TCTGAATCTGGTTCAGAGTCAGGCAGTCAATCCGAATCAGAGTCTGACACATCTAGAGAG
                                                                                                                                                                                                                                                                                                         441 AAGAAACAAGTTCAAGCTAAACCTCCGAAAGCTGACGGATCTGAGTTTTGGAAGTCCAGT
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Qy Db	2352 CAAATTCTGAGGATGGAATGAGTGCAFTGCAGAAGCAATATTACAAGTGGATTTAACA 2411
Qy	2412 AGGAATTATAAAGCCCTCAGTAAAGGTTCAAAAGGGGGGTACCTCAGGCTTTCTGAACATT 2471
Oy Db	TTGCTACCTCATTAA TTGCTACCTCATTAA
Qy	532 GAATTCTATAATAAACAGGAGGCCTTACAGCATTTGATACGTACG
Qy	592 CITCITGACAAGCTACIGATTGGCGAGAACGTGCCACAAGAGTTCIGAITTTCICT 26
Oy Db	652 CAGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTATCGCCAGTTTCCCTTC 27
Oy Dp	39TCAATAAAAGGGAATTGAGGAAGCAAGCACTGGATCATTTCAAT 27
Qy Db	ATTICTGTTTTTACTGTCTACAAGAGCTGGAGGATTAGGTATT 28
Qy	SACACTGTAGTTATTTTGATTCTGACT
Qy Dp	2892 CTGCAGGCACAGGCGAGAGCTCATAGAATTGGACAGAAGAAACAGGTTAATATTTATCGG 2951
Qy Db	2952 CTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAAGAAGAAGATGGTG 3011
Qy Db	STARTTCAGAGAATGGACACGACAGGAAAACTGTTCTGCATACAGGT
Qy	AAGCTCTACACCTTTTAATAAAGAAGAGTTATCAGCTATTTTGAAGTT 313
Qy Db	TTAAAGAACCTGAAGGAGAAGAACAGGAGCCCCAGGAAATGGAT 31
Oy Db	aagagagctgaaactcgggaaaatgagccaggtccattgactgta 325
Qy Db	TTTCACAGTTCAAGGTGGCGAACTTTTCCAATATGGATGAAGATGAT 33
Qy Db	AGAAAGAAATTCAAGAAATTGGGAAGAAATCATCCCCAGAATCCCAA 337
Qy	IGGAGGAGGAACACAAAAGAACTTCAAGAATATACATGCTCCCG 34
į	24.30 NGCARCANAAACHGCAAAAAAAAA

Mon Aug

AGARGAGAACTGTCCAAAGCAGATAACTTCAATGGAAGGGAGGG

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07-AUG-2001
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Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
AF181826
2943 bp mRNA linear VRT 07-AN Gallus gallus chromosome W chromodomain helicase DNA binding procesin 1 (CHDIW) mRNA, partial cds.
                       5286 TCTCCTTATGGTTCAAGATCTCCCCTAGGACACAGATCTCCATTTGAACACTCATCAGAT
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Pridolfsson, A.-K. and Ellegren, H.
Fridolfsson, A.-K. and Ellegren, H.
Submitted (30-AUG-1999) Department of Evolutionary Biology,
Evolutionary Biology Centre, Uppsala University, Norbyvagen 18D,
Uppsala S-75236, Sweden
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Aegolius funereus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Fridolfsson, A.K. and Ellegren, H.
Molecular evolution of the avian CHD1 genes on the Z and W sex
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2 (bases 1 to 2754)
Fridolfsson,A.-K. and Ellegren,H.
Fridolfsson,A.-K. and Ellegren,H.
Direct Submission
Submitted (30-4007) Department of Evolutionary Biology,
Evolutionary Biology Centre, Uppsala University, Norbyvagen 18D,
Uppsala S-75236, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2581 TGCATTAAGGCTTTAAATGATAATGACTTTGGTCAAGGAAGAACAGGTGGTAGATTTGGG
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losome 2 chrom
partial cds.
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Genetics 155 (4), 1903-1912 (2000)
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Aegolius funereus chromosome
protein 1 (CHD12) mRNA, parti
AF181825 GI:5917749
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NPONIO AGARARRI GOKKON NI TRI JYTKGSY BEDLI ERAKKKKULDIL VI OKADOTO KTULHI GSTPSSET PENKEDI. SALIKRO AGELEK BEDEGEORO BOLD IDELI KRABTR ENBEPPI JYDKOBELLSOFKVAN PESHADBODI ELEPENSHWEET I PEPURATRI ERBER OKELEET YML PRARNCAKOI SFNGSEGRRSRSRRY SGSDSOSI SERKRPKKRGRPT I PRENTKGESDAELTRET KYSKYKGFOF LENDAYRADAEL TVOK STOLD FARLAELTHING IKALKDSSSOGRAGGERGGENGKYKGPTFRI SGYQYUNALL I SHEBELAPLIKS I PSDPPE RKRY I PCHTKAARFDI DMGKEDDSNLLIGITY SYGYGSWEMI KMDPDLLSLTOKILD DD ILRUBNSALOKOY VWILTRINYKALSKGSKGSTSGFLANIMBELKKCOHCYLIK PPÖG NEFVINKOBALQHLIRSSGKLILLIDKLIRLERGRINVLIFSOMPMILLABYLKTRO PPORLOGSIKKELKROALOHFRARGSBEPCFLLSTRAGGLGTRIASADTVITESDM ö JKDKSFLGGLNWAFIGVDEAHRLKNDDSLLYKTLIDFKSNHRLLITGTPLQNSLKELW SLLHFIMPEKFSSWEDFEEEHGKGREYGYASLHKELEPFLLRRVKKDVEKSLPAKVEQ 1353 GAGCTTACAGATGATCTGCACAAACAATATCAAATAGTGGAAAGAATAATTGCTCATTCA 1412 1413 AATCAAAAGTCAGCAGCTGGTTATCCGGACTATTGCAAATGGCAGGGTCTGCCTTAC 1472 1473 TCAGAATGTAGCTGGGAAGATGGTGCTCTCATTGCCAAAAAGTTTCAGGCACGCATTGAT 1532 1533 GAGTATTTTAGCAGAAATCAATCCAAGACTACTCCCTTTAAGGACTGCAAGGTTCTAAAA 1592 1593 CAGAGACCAAGATTTGTTGCACTGAAGAAGCAACCATCTTACATTGGAGGACATGAAAGT 1652 GTAGTTTACTTAGGAGATATAACTAGTAGAAATATGATAAGGACTCATGAATGGATGCAT 1952 CCACAGACTAAACGATTAAAGTTTAACATACTTCTGACGACATATGAAATTTTACTGAAG 2012 GATAAGTCATTCCTTGGTGGTCTCAATTGGGCATTCATAGGAGTTGATGAAGCTCATCGT 2072 TTAAAAAAATGATGACTCTTCTTTCTGTACAGGACTTTAATAGACTTTAAGTCCAACCATCGA 2132 1773 TTTCTGAACTACCTGTTTCATGAACATCAACTGTATGGCCCTTTTCTTCTGCGCGTGCCA 1832 CTTTCTACCTTGACATCTTGGCAAAGAGAGATTCAAACTTGGGCTCCTCAGATGAATGCT 1892 61 AATCAGAAATCGGCGGCTGGTTATCCAGACTACTATTGTAAATGGCAGGGTCTGCCGTAT 120 421 ITTCTGAACTACCTGTTTCACGAACATCAGTTGTATGGGCCTTTCTTGCTGGTCGTGCCA 480 Gaps 1 GAGCTTACAGATGATCTACATAACAATATCAGATAGTGGAAAGAATAATTGCTCATTCA 60 Query Match 37.2%; Score 2458; DB 5; Length 2754; Best Local Similarity 93.3%; Pred. NO. 0; Matches 2569; Conservative 0; Mismatches 185; Indels 0; 706 t 636 g 481 c ď 931 BASE COUNT ORIGIN 1953 601

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2552 2612 2193 TTCATCATGCCAGAAAATTTTCCTCCTGGGAAGATTTTGAAGAGGAGCATGGCAAAGGA 2252 2253 AGAGAGTATGGTTATGCAAGTCTTCACAAAGAGCTTGAACCATTTTTACTAAGAAGAGTT 2312 2313 AAAAAAGATGTAGAAAAGTCTTTACCTGCTAAGGTTGAACAAATTCTGAGGATGGAAATG 2372 2373 AGTGCATTGCAGAAGCAATATTACAAGTGGATTTTAACAAGGAATTATAAAGCCCTCAGT 2432 2433 AAAGGTTCAAAAGGCAGTACCTCAGGCTTTCTGAACATTATGATGGAACTTAAGAAGTGT 2492 2613 CGTCTGCGAGAACGTGGCAACAGAGTTCTGATTTTCTCTCAGATGGTGAGGATGCTGGAC 2672 2673 ATCCTAGCAGAATATCTGAAGTATCGCCAGTTTCCCTTCCAGAGACTTGATGGATCAATA 2732 2733 AAAGGGGAATTGAGGAAGCAAGCACTGGATCATTTCAATGCAGAAGGATCAGAGGATTTC 2792 2793 IGITITITACIGICIACAAGAGCIGGAGGATTAGGIATTAACIIGGCAICIGCIGACACI 2852 1441 TGCTTTTACTGTCTACCAGAGCTGGAGGATTAGGTATCAACTTGGCATCTGCTGCTGACAT 1500 2853 GTAGTTATTTTGATTCTGACTGGAATCCACAGAATGATCTGCAGGCCACAGGCGAGAGCT 2912 2913 CATAGAATTGGACAGAAGAACAGGTTAATATTTATCGGCTAGTCACAAAAGGATCAGTA 2972 2973 GAAGAAGATATTCTTGAAAGAGCCAAGAAGAAGATGGTGCTAGACCATTTAGTAATTCAG 3032 3033 AGAATGGACACGACAGGAAAAACTGTTCTGCATACAGGTTCAACTCCATCAAGCTCTACA 3092 CCTTTTAATAAAGAAGAGTTATCAGCTATTTTGAAGTTTGGTGCTGAGGAACTCTTTAAA 3152 3153 GAACCTGAAGGAGAAGAACAGGAGCCCCAGGAAATGGATATAGATGAAATCTTGAAGAGA 3212 3213 GCTGAAACTCGGGAAAATGAGCCAGGTCCATTGACTGTAGGGGATGAGTTGCTTTCACAG 3272 901 AGAGAGTATGGTTATGCAAGTCTTCACAAAGAACTTGAACCATTTCTGTTGAGAAGAGTT 960 2493 TGTAACCATTGCTACCTCATTAAGCCACCAGATGATAATGAATTCTATAATAACAGGAG GCCTTACAGCATTTGATACGTAGCAGCGGGAAACTAATCCTTCTTGACAAGCTACTGATT 2553 q ò a ò QQ δ ద à g ò q ò g Ω Ω Q.y D.b 5 6 δy g ò ò ద ò qq δ οg ò 8 à 8 Q οy ò

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LSTTTSWQREIGTWASGWANTYLGITTSRNAITFHEWHIPOTRILLETTYELL
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                                                                                                        2. (bases 1 to 2754)
Fridolfsson, A.-K. and Ellegren, H.
Fridolfsson, A.-K. and Ellegren, H.
Submission
Submission
Submitted (30-AuG-1999) Department of Evolutionary Biology, Centre, Uppsala University, Norbyvagen 18D, Uppsala S-75216, Sweden
Location, Qualifiers
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Pred. No. 0;
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    Molecular evolution of the avian CHD1 chromosomes Genetics 155 (4), 1903-1912 (2000)
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1 (bases 1 to 2754)
Fridolfsson, A.K. and
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Best Local Similarity 93.33
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TITLE
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Ekaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Psittaciformes; Cacatuidae;
Nymphicus.
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binding protein 1 (CHD12) mRNA, partial cds.
AF181828
                                                                             CCTCCAGAAAATATTAAAGGATTTAGTGATGCAGAGATCAGGGGGGTTATCAAGAGTTAC
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                                                         TTCAAGGTGGCGAACTTTTCCAATATGGATGAAGATGATATTGAGTTGGAACCAGAAAGA
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1740 3152 AAATGAGCCAGGTCCATGACTGTAGGGGATGAGTTGCTTTCACAG 3272 2160 3572 3812 2852 1500 2912 2972 1620 3032 3092 AGAACAGGAGCCCCAGGAAATGGATATAGATGAAATCTTGAAGAGA 3212 SGAAGAAATCATCCCAGAATCCCAACGGAGAAGGATAGAGGAGGAG 3392 regeagteaagaagacecagtaggagcagaagatattctggatct 3512 PAAAGGATTTAGTGATGCAGAGATCAGGCGGTTTATCAAGAGTTAC 3632 CCTCTGGAAAGGTTAGATGCTGTAGCTAGAGATGCTGAACTGGTT 3692 AGACCTTAGACGTTTGGGTGAACTTGTACATAATGGATGCATTAAG 3752 IGAAAGAGCCAAGAAGAAGATGGTGCTAGACCATTTAGTAATTCAG AGGAAAAACTGTTCTGCATACAGGTTCAACTCCATCAAGCTCTACA AGAGTTATCAGCTATTTGAAGTTTGGTGCTGAGGAACTCTTTAAA CACAGAAAGAAACGGCCAAAAAGCGTGGAAGACCTCGAACCATT **FTCATCTGGACAAGAAGAGCAGGAGGTAGACTTGGGAAAGTTAAA** TACAAGAGCTGGAGGATTAGGTATTAACTTGGCATCTGCTGACACT PTCTGACTGGAATCCACAGAATGATCTGCAGGCACAGGCGAGAGCT SAAGAAACAGGTTAATATTTATCGGCTAGTCACAAAAGGATCAGTA

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LKDK SFLGGLINWYF I CYDABLARLKNDDS LLYKTHEWMHPOTKRLK FULLLYTYELL
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SLJHFI IMPEKESSWEDFEEBEIGK GREFGY SSTHKELEPFLLRRYK KNDYEK SLEW FOR
I LRMEMSALOKOYYKWI LTRNYKALSKGSKGST GFLNI MMELKKCCNHCYLIK PDD
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NPONDLOAOARAR RI CÓRKOYNI Y RLYTKGSYBEDI LERRKKKWLDHLY I ORWOTTG
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IKALKDNSFGQERAGGRLGKVKGPTFRISGVQVNAKLVISHEEELAPLHKSIPSDPED
RKRYVIPCHTKAAHFDIDWGKEDDSNLLIGIYEYGYGSWEMIKMDPDLSLTQKILLPDD
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chromodomain helicase DNA binding
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Fridolfsson, A. K. and Ellegren, H. Molecular evolution of the avian CHD1 genes on the Z and W sex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tridolfsson, A.-K. and Ellegren, H.
Fridolfsson, A.-K. and Ellegren, H.
Direct Submission
Submitted (30-AUG-1999) Department of Evolutionary Biology,
Evolutionary Biology Centre, Uppsala University, Norbyvagen 18D,
Uppsala S-75356, Sweden
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                 3993 TCCAATCTGTTAGTAGCCATCTATGAATATGGCTATGGCAGCTGGGAAATGATAAAAATG
                                                                                                                                               GTCATCCCATGCCACACACCAAGGCTGCTCACTTCGATATAGATTGGGGTAAAGAAGATGAT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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/db_xref="taxon:103375"
/chromosome="W"
<1. .>2754
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Aegolius funereus chromosome W chrom
protein 1 (CHDIW) mRNA, partial cds.
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                                                                                                     AATCAAAAGTCAGCTGGTTATCCGGACTACTATTGCAAATGGCAGGGTCTGCCTTAC
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      2754;
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0
      Length
      5
                                          207;
      DB
Score 2422.8;
Pred. No. 0;
0; Mismatches
  36.7%;
llarity 92.5%;
Conservative
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  Query Match
Best Local Simi
Matches 2547;
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AGTGCATTGCAGAAGCAATATTACAAGTGGATTTTAACAGGAATTATAAAAGCCCTCAGT	CGTCTGCGAGAACGTGGCAACAGATCTGATTTCTCTCAGATGGTGAGGATGGTGGAGCCTGGACCTGTGACCTGGAACGTTGTGATTTTCTCTCAGATGGTGAGGATGCTGGACCTTGAGATGTTGAGATGTTAGAGATGATGAGATGATGAGATGAT	TGTTTTTACTGTCTACAAGAGCTGGAGGATTAGGTATTAACTTGGCATCTGCTGACACT TGTTTTTACTGTCTACCAGGGTGGAGGATTAGGTATAACTTGGCATCTGCTGACACT TGCTTTTTGCTTACTACTGAGGTGGAGATTAGGTATAACTTGCAGCGTGCTGACACT GTAGTTATTTTGGATCTGACTGGAATCCACAGATGATCTGCAGGCGACACGCTGTTTTTTTT	GAAGAAGATATTCTTGAAAGAGCCAAGAAGATGGTGGTGGACCATTTAGTAATTCAG [
2373 1021 2433 1081 2493 1141 2553	2613 1261 2673 1321 2733 1381	2793 1441 2853 1501 2913 1561	2973 1621 3033 1681 3093 1741	1801 3213 1861 3273 1921 3333 2041
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Psittaciformes; Cacatuidae;
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2 (Dates 1 to 2754)

Friedifisson, A. K. and Ellegren, H.

Direct Submission

Submitted (30-AUG-1999) Department of Evolutionary Biology,

Evolutionary Biology Centre, Uppsala University, Norbyvagen 18D,

Uppsala S-75236, Sweden

Location/Qualifiers
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                                                                     3513 GATAGTGACTCCATCACAGAAAGAAAACGGCCAAAAAAGCGTGGAAGACCTCGAACCATT 3572
                                                                                           3573 CCTCGAGAAAATATTAAAGGATTTAGTGATGCAGAGATCAGGCGGTTTATCAAGAGTTAC 3632
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Fridolfsson, A. K. and Ellegren, H.
Molecular evolution of the avian CHD1 genes on the Z and W sex
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Nymphicus hollandicus chromosome W chromodomain helicase DNA
binding protein 1 (CHDIW) mRNA, partial cds.
AF181827
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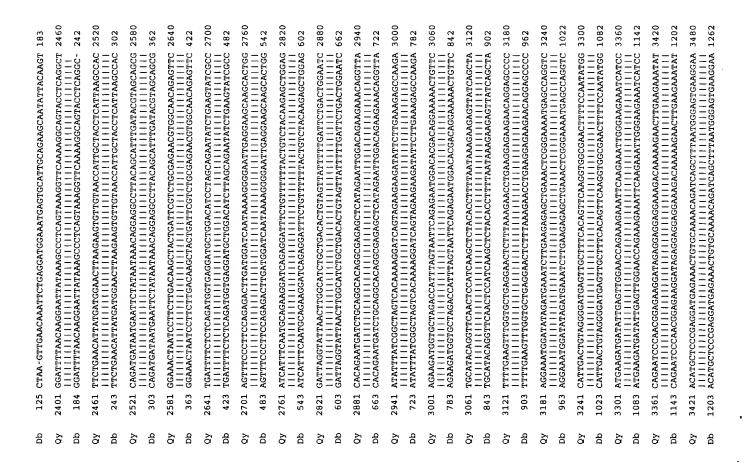
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                              3033 AGAATGGACACGACAGGAAAAACTGTTCTGCATACAGGTTCAACTCCATCAAGCTCTACA 3092
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Submitted (29-JAN-1993) Jun-ichi Funahashi, Inst. Devel., Aging and
Cancer, Tohoku Univ.; 4-1 Seirvo-machi, Abba-ku, Sendai 980-77,
Jappan (Tel.1022-272-9499, Fax:022-272-3982)
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/db.zref="dI:391400"
/db.zref="dI:391400"
/fb.zref="dI:391400"
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VTKGSVERDILERAKKKMYLDHVIQNKOTTGKTVUHTGSTPSSSTPFNKEELSAILK
FGAEELFKEPEGEEQEPQENDIDEILKRAETHENEPGPLIVGDELLSQFKVANFSNND
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GRRSKSRRYSGSDOSITERAKRAKRARITIRENIK KESDALIRERIK KSYKERGE
LERLDAVARDASLUNKSETDIRLGELVINGCIR LAKDNSSOGERAGGELOKKOFP
RIGSOVANAKLVISHERELAPLIKSIFSOPERRKRYVICHTKAAHPDIDNGKEDDSN
LIVGIYEYAKGSWOÇXVIGSRSOLNITEII.PDDDPRTPRONSYRPVQTTSLNY"
385 c 546 g 534 L
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                                             VRT 03-FEB-1999
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//note="beta-gal fusion protein binds to blocks 10 to 3 of
HN fragment of delta-crystallin enhancer."
                                                                                                                                                                                                                                       Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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                                                                                                                                                           Gallus gallus (library: lambda gtll) 13 day embryo lens cDNA
mRNA, clone JFll.
Gallus gallus
                                          D14316 arnoar VRT 03-FF D14316 linear VRT 03-FF delta-crystallin enhancer binding protein, complete sequence
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/clone_lib="lambda gtll"
/dev_stage="13 day embryo"
257. .1939
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Location/Qualifiers
L. 2292
/ Organism-"Gallus gallus"
/db_xref="taxon:9031"
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Funahashi,J.
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1 (bases 1 to 2292)
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D14316.1 GI:391639
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4437 2100 1921 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAGTCGCTAAAAGGCTTGCTG ATGCAGAGATCAGGCGGTTTATCAAGAGTTACAAGAAATTTGGTGGCCCTCTGGAAAGGT ATGGCTATGGCAGCTGGGAA-ATGATAAAAATGGATCCAGATCTCAGCTTAACACAGAAG ATGCCTATGGCAGCTGGCAATGTAAAGTAAATGGATCCAGATCTCAGCTTAACACAG-AG GTGCAGGCAATTCCAAGAGAAGAAGACAAGAATAAGAAGAATAAGAATAAGATTGAA AAAAAATTCCATTGCTGGATACTCCAGTTCATATTACTGCAACCAGTGAACCAGTTCCTA ATGCAGAGATCAGGCGGTTTATCAAGAGTTACAAGAAATTTGGTGGCCCTCTGGAAAGGT TAGATGCTGTAGCTAGAGATGCTGAACTGGTTGATAAATCTGAGAGACGGACCTTAGACGTT TGGGTGAACTTGTACATAATGGATGCATTAAGGCTTTAAAGGACAATTCATCTGGACAAG **AAAGAGCAGGAGGTAGACTTGGGAAAGTTAAAGGCCCCAACGTTTCGAATCTCAGGAGTGC** AGGTGAATGCAAAACTAGTCATCTCTCACGAAGAAGAGGCTGGCACCACTGCAAAATCCA TTCCTTCAGATCCAGAAGAAAGGAAAAGATATGTCATCCCATGCCACACCAAGGCTGCTC ACTTCGATATAGATTGGGGTAAAGAAGATGATTCCAATCTGTTAGTAGGCATCTATGAAT TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAG--CACAAAGGCTTGCTG **AAATAAAAGAAGAAATAAAGAGTGATTCTTCACCACACACCCTCAGAAAATCTGATGAAG** ATTTTACCTGATGATCCAGACAAGAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGAC GGCCTGTCAAAG 4509 1683 4080 1862 2101 2161 1323 1383 1503 3781 1563 3841 1623 1743 4021 1803 4140 4198 4258 2041 4318 3601 3661 3901 4378 4438 3541 3721 3961 1981 2221 g δ g ò g δ g Qγ g δ g δŽ 염 ò Dp ŏ g Qγ Db òγ g δ Db δy g ŏ Dp δy qq ò Ω δý a à Qγ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MMRNKDKSQEEDSSLHSNASSHSASEEASGSDSGSQSESEQGSD
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KSKRSQGPVHITAGSEPVPIGEDEDDDLDQETFSICKERWRPVKKALKQLDKPDKGLN
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WYKDHHYGDRRHMDAHRSGSYRPNNMSRKRPYDQYSSDRDHRGHRDYYDRYAKGCETP
                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I sto Arain, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins

Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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KMAHKRRSQEEEEQKKKDDVTGGKKPPRPEASGSSRDSLISQSHTSHNLHPQKPHLPA
                                                             PRI 27-NOV-1997
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/db_xref="taxon:9606"
/chromosome="15"
/map="15q26; between WI-6813 and D15S157"
                                                             linear
                                                             mRNA
                                               7764 bp mRR
Homo sapiens CHD2 mRNA, complete cds.
AF006514
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708, 5927
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Submitted (03-JUN-
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RESULT 11
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23.0%; Score 1522; DB 9; Length 7764;

Query Match

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Best Local Similarity 63.2%; Pred. No. 6.5e-310;
Matches 2672; Conservative 0; Mismatches 1335; Indels 219; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   951 GCTGAAGAAACCAAGACAGATTCTGATGATTTGCTGGAAGTTTGTGGAGAGGATGTCCCA 1010
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                                                                          717 TCGGCGGAAGATGGGGATAAAAGCAGTTGTGAAGAAAGTGAATCTGACTATGAGCCAAAA 776
                                                                                                                                                                            777 AACAAAGTCAAAAGCCGTAAACCTCCAAGCAGAATTAAGCCAAAAAGTGGGAAAAA---- 832
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3504 AIGGTATTAGATCATCTGGTGATTAGCGCATGGACACCACTGGCCGGACGATCGTGGAA 3563 3800 3365 ATGGATATAGATGAAAATCTTGAAGAGGTGAAACTCGGGAAAATGAGCCAGGTCCATTG 3245 4154 3126 AAGTTTGGTGCTGAGGAACTCTTTAAAGAACCTGAAGGAGAAGAACAGGAGCCCCCAGGAA 3185 ACTGTAGGGGATGAGTTGCTTTCACAGTTCAAGGTGGCGAACTTTTCCAATATGGATGAA 3006 ATGGTGCTAGACCATTTAGTAATTCAGAGAATGGACACGACAGGAAAAACTGTTCTGCAT GATGATATTGAGTTGGAACCAGAAAGAAATTCAAGAAATTGGGAAGAAATCATCCCAGAA 3801 GAAGAA-----GAGCTAGAAGAGCGTCCTCACAAGGACTGGGATGAGATCATTCCAGAG GGAAGACGCAGTAGGAGCAGAAGATATTCTGGATCTGATAGTGACTC-----CATCACA GAAAGAAAACGGCCAAAAAAGCGTGGAAGACCTCGAAACCATTCCTCGAGAAAATATTAAA 3822 TTTCGAATCTCAGGAGTGCAGGTGAATGCAAAACTAGTCATCTCTCACGAAGAAGAGCTG ACAGGTTCAACTCCATCAAGCTCTACACCCTTTTAATAAAGAAGAGTTATCAGCTATTTTG 3366 TCCCAACGGAGAAGGATAGAGGAGGAGGAAGACAAAAAGAACTTGAAGAAATATACATG 3426 CTCCCGAGGATGAGAACTGTGCAAAACAGATCAGCTTTAATGGGAGTGAA-----3915 CIGCCICGAATICGGAGIICCACIAAAAAGGCICAGACAAAIGACAGIGACICIGACACI 4035 GATGACAAGAAGCCAAAAGCGCAGAGGGCGTCCGAGGAGTGTGCGGAAGGACCTCGTGGAG 3711 CTTAGACGTTTGGGTGAACTTGTACATAATGGATGCATTAAGGCTTTAAAGGACAATTCA -----TCTGGACAAGAAGAGCAGGAGGTAGACTTGGGAAAGTTAAAGGCCCAACG 3246 3384 3066 3564 3186 3306 3477 3975 3531 2886 3651 3771 qq g g ò q ò g ò qq δ g QY a δ Q οy qq QQ g ΩD g g g g οy Ω à δ οχ ŏ δ ŏ δ 셤 ò

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GILITITHS, R. and Tiwari, B. AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS 2943 ATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGGCCAAGAAG 3002 3003 AAGATGGTGCTAGACCATTTAGTAATTCAGAGAATGGACACGACAGGAAAAACTGTTCTG 3062 3063 CATACAGGTTCAACTCCATCAAGCTCTACACCTTTTAATAAAGAAGAGTTATCAGCTATT 3122 3183 GAAATGGATATAGATGAAATCTTGAAGAGCTGAAACTCGGGAAAATGAGCCAGGTCCA 3242 3243 TTGACTGTAGGGGATGAGTTGCTTTCACGTTCAAGGTGGCGAACTTTTCCAATATGGAT 3302 3303 GAAGATGATATTGAGTTGGAACCAGAAAGAAATTCAAGAAATTGGGAAGAAATCATCCCA 3362 3543 CCAAAAAAGCGTGGAAGACCTCGAACCATTCCTCGAGAAATATTAAAGGATTTAGTGAT 3602 121 CATACAGGCTCTACTCCTTCAAGCTCAACACTTTTAATAAGGAAGAGTTATCAGCAATT 180 1 ATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAATATTCTTGAAAGAGCCAAGAA 60 0; Gaps

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SEQUENCING IN PROGRESS ***, in ordered
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Oualifiers
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyeera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 14530)
Adams, M. and Venter, J.C.
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Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
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Length 14530
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Score 867.4; DB 2;
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On Jun 9, 1999 this sequence version replaced gi:3293203
gi:3097820.
gi:3097820.
Berkeley brosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Pl library locations: 23-78, 10-42.
2 (bases 1 to 163403)
Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butchhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,R.A., Hummasil,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Svirskas,R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1077 GCCACTGGTGCCTCAACCACCATCTATGCCGTTGAGGCAGATGG---TGACCCAAATGCT 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1134 GGGTTTG------AAAAGTCAAAGGAGCTGGGAAAATACAGTATCTTATTAAATGG 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGGCTGGTCACACATCCATAACACTTGGGAAACTGAAGAAACGCTGAAGCAACAAAAT 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTAAAGGAATGAACAAACTGGACAACTACAAGAAAAAGGATCAGGAGACAAAACGCTGG 1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="23C1-23C5"
/clone="Pls DS02190 (D82) and DS00906 (D99)"
/clone_lib="Pl library, partial Sau3A in pAd10sacBII"
1 35896 c 36551 g 45750 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 174; Gaps
                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (09-JUN-1999) Berkeley Drosophila Genome Project, M
64-121, Lawrence Berkeley National Laboratory, One Cyclotron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAAAAATGCTTCTCCAGAAGATGTGGAATATTATAACTGCCAGCAGGAGCTTACAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 163403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berkeley, CA 94720, US
On Jun 9, 1999 this sequence version replaced gi:3293203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/strafin="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 867.4; DB 3;
Pred. No. 4e-172;
0; Mismatches 1571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.1%;
Best Local Similarity 55.0%;
Matches 2134; Conservative
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ORIGIN
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AC007765 AC004375 AC00231 AC003633 AC003634 AC003635 AC004154 AC002028 AC002029 AC002977 AC002031 AC002031 AC002032 AC002031 AC002031 AC002032 AC002033 AC002033 AC002031 AC002032 AC002033 AC002033 AC002033 AC002033 AC002033 AC002035 AC0
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1 (Dases 1 to 16340)
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff C., Champe, M., Chavez, C., Chew, M., Clasiolka, L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Käin, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Fefiffer, B., Seon, J., Sequeira, A., Sethi, H., Snir, E., Sarirs, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4403
                                                                                                                                                                                                                                                                                                                                                                                                            2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCACAACCCTCAGAAA----AATCTGATGAAGATGATGAGGAGGAGGAGGATAACAAGGTA 4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2164 ACCGCGTCGCCGCACAATGCTCCAGCTACGGAACAGCACGGTGACCCTGCGAAGAAAGCC 2105
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                                                                                                                                                                                                                                                 2284 GCCAAGGCGGCAAGCCAGTCTGCTTCGACCATGGTGGTAAGCCGCACGATGGGGAG
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                                                                                                         2344 GAGCTGACCAAGGGAGGACAACGCCGACAACGGCGCCCCAGAGCATCGCGAGCTAACGAT
                                                                                                                                                                                     AATGAAATGAAATCTGAAAATAAAGAAAATCTAAAAAATTCCATTGCTGGATACTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4404 GTTCATATTACTGCAACCAGTGAACCAGTTCCTATCTCAGAAGAATCTGAAGAACTCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4704 AGAAAGCTGCACAAACTCTACAAACATGCAATCAAAAG 4742
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46543 GGTACCCCGCTGCAGAATICGCTGAAGGAGCTCTGGGCTTTGCTGCACTTCATCATGCCG 46602 46009 TTCTCTCGAATAAAGAATCAGCCGGAATTTCTTTCGTCGGCCCTAACTC-----TAAGG 46062 46663 TACACTCGGTTGCATCAACAGCTGGAGCCGTATATTCTGCGGAGAGTGAAGAAGGATGTG 46722 45949 CGCGAGTCCTCCAAATGCACTCCCTCCCGCCACTGCAGAGTGATCAAGTATCGCCCCAAG 46008 CGATTAAAGTTTAACATACTTCTGACGACATATGAAATTTTACTGAAGGATAAGTCATTC 2024 1605 TTTGTTGCACTGAAGAAGCAACCATCTTACATTGGAGGACATGAAAGTCTGGAGTTAAGA 1664 CTGTTTCATGAACATCAACTGTATGGCCCTTTTCTTCTGCGCGTGCCACTTTCTACCTTG 1844 GGAGATATAACTAGTAGAAATAFGATAAGGACTCATGAATGGATGCATCCACAGACTAAA 1964 CTTGGTGGTCTCAATTGGGCATTCATAGGAGTTGATGAAGCTCATCGTTTAAAAAATGAT 2084 GACTCTCTTCTGTACAGGACTTTAATAGACTTTAAGTCCAACCATCGACTTCTGATTACT 2144 GGAACCCCACTGCAAAATTCCCTCAAAGAGCTGTGGTCTTTGTTGCATTTCATCATGCCA 2204 2205 GAAAAATTTTCCTCCTGGGAAGATTTTGAAGAGGAGCATGGCAAAGGAAGAAGTATGGT 2264 2265 TATGCAAGTCTTCACAAAGAGCTTGAACCATTTTTACTAAGAAGAGTTAAAAAAGATGTA 2324 2325 GAAAAGTCTTTACCTGCTAAGGTTGAACAATTCTGAGGATGGAAATGAGTGCATTGCAG 2384 2385 AAGCAATATACAAGTGGATTTTAACAAGGAATTATAAAGCCCTCAGTAAAGGTTCAAAA 2444 2445 GGCAGTACCTCAGGCTTTCTGAACATTATGATGGAACTTAAGAAGTGTTGTAACCATTGC 2504 2505 TACCTCATTAAGCCACCAGATGATAATGAATTCTATAATAAACAG---GAGGCCTTACAG 2561 1545 AGAAATCAATCCAAGACTACTCCCTTTAAGGACTGCAAGGTTCTAAAACAGAGCCAAGA 1604 1845 ACATCTTGGCAAAGAGAGAGATTCAAACTTGGGCTCCTCAGATGAATGCTGTAGTTTACTTA 1904 1485 TGGGAAGATGGTGCTCTCATTGCCAAAAAGTTTCAGGCACGCATTGATGATGATTTTAGC 1544 2085 (1785 2025 g g δ qq ò g ŏ qq oy Op ò Q ò g ŏ g o QQ ò q õ q ò q ð qq ŏ 8 ò 엄 à

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ROJL, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,

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Radele, J., Smith, H.O., Rubin, G.M. and Venter, J.C.

Saquencing of Drosophila chromosome 2L, region 23E-23F

Unpublished

Callson, J.W., Champe, M., Damantides, P.G., Brandon, R.C.,

Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,

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Rapeleton, M., Strong, R., Swirskas, R., Tector, C., W
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Drosophila melanogaster, chromosome 2L, region 23E-23F, BAC clone
BACR38N06, complete sequence.
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Submitted (26-UNN-2001) Berkeley Drosophila Genome Project, MS
64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, US
Sequence submitted by:
Berkeley prosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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Chicken CHD-W gene
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Drosophila melanog
DNA encoding novel
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Tiwari B;

Griffiths R,

100.0 16.6 13.1 13.1 8.4 4.9 4.7 4.7

867.4 867.4 553.2 321.4 311.2 309.6

Score

Result No. 1098.

WPI; 1997-043127/04.

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The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo CDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or 2 chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. Of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                         ŗ
                 chromodomain-helicase-DNA binding genes determine sex \cdot used for sex determn. and to control sex of progeny
                                                                                           Claim 1; Fig 5; 76pp; English
                      Avian
                                             birds
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Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;

ö 120 CAAGTCAAACGCATTACTTCGAAAACATACGGAGTACCAGAAAGGGGATTCTTGACCTAC 180 caagtcaaacgcattacttcgaaaacatacggagtaccagaaaggggattcttgacctac 180 240 300 GGTCAGCTTCAGGTTCTGGATCTGGTTCAAGCTCTGGAAGCAGTAGCGATGGAAGTAGCA 360 360 GCCAGTCAGGTAGCAGTGACTCTGAATCTGGTTCAGAGTCAGGCAGTCAATCCGAATCAG 420 420 480 480 540 540 909 009 99 099 CCGCCGAGCCGGACGCACGCAGGTATTTGGGCAAAAATCTTGGCCATCTGTAGAGAATAG 120 Gaps 9 9 CGGGCTGCGGCACGAAGCGCACCGCCGGCGCACGCAGGCTCGGGCCGGGGAAGGCCTGGC cgggctgcggcacgaagcgcaccggcggcacgcaggctcggggccggggaaggcctggc GTGATGAAGAAAGTGTAAGAAACAGCAGTGGAGAGTCAAGCAGATCAGATGATTCTG **AGTCTGACACATCTAGAGAGAAGAAACAAGTTCAAGCTAAAACCTCCGAAAGCTGACGGAT** CTGAGTTTTGGAAGTCCAGTCCAAGCATACTTGCTGTACAGAGATCAGCAGTGCTCAAGA AGCAACAGCAACAGCAAAAAGCAGCATCATCAGACAGTGGTTCAGAAGAGGACTCATCCA DB 18; Length 6608; ; 0 Indels ; 0 0; Mismatches 100.0%; Score 660%; 100.0%; Pred. No. 0; Conservative Best Local Similarity Matches 6608; Conser Query Match 61 121 241 541 61 121 181 181 241 301 361 361 421 481 541 601 199 301 421 481 601 661 g δ d g δy g ŏ g οŽ Db Qy QQ ò g οy g ò 8 ò a ò

1 CGGAAGATGG 1	GGATAAAAGCAGTTGTGAAGAAAGTGAATCTGACTATGAGCCAAAAAACA 780 	CCGTAAACCTCCAAGCAGAATTAAGCCAAAAAGTGGGA 	3AGGCAACTTGATTCATCAGAGGAGGAGGAGGACGAI 	ATCTCGTCGCCAGGCAACAGTGAATGTTAGTTACAAAGAAGCT. 	ITCTGATGATTTGCTGGAAGTTTGTGGAGAGGATGTCCCAC 	roaaactatagagaagtttatggacagtcgaattggccgaaaaggagcc 	AACCACCATCTATGCCGTTGAGGCAGATGGTGACCCAAA 	GCTGGGGAGAATACAGTATCTTATTAATGGAAAGGCTGGTCACAC. 	SGGAAACTGAAGAAACGCTGAAGCAACAAAATGTT 	TRCAAGAAAAAGGATCAGGAGACAAAAGGCTGGCTGAAAAATGC 	GGAATATTATAACTGCCAGCAGGAGCTTACAGATGAT 	GGAAAGAATAATTGCTCATTCAAATCAAAAGTCAGCAGCT 	CAAATGGCAGGTCTGCCTTACTCAGAATGTAGCTGGGAA 	AGTTTCAGGCACGCATTGATGATGAGTATTTTAGCAGAA 	NGGACTGCAAGGTTCTAAAACAGAGACCAAGATTTGTT 	TTACATTGGAGGACATGAAAGTCTGGAGTTAAGAGATTATCAGTTAAAT 	GCTCGCTCATTCATGGTGCAAAGGAAATAGTTGTATTCTT 	TAAAACAATACAAACAATTTCTTTTCTGAACTACCTGTTTCTT 	
	21 CGGAAGATGGGGATAAAAGC 	81 AAGTCAAAAGCCGTAAACCT 	41 GACAGAAGAAGAGGCAACT 	01 ATAAGAGAGGATCTCGTCG 	61 CCAAGACAGATTCTGATGAT 	21 AAGATGAATTTGAAACTATA 	81 CTGGTGCCTCAACCACCAT 	41 AAAAGTCAAAGGAGCTGGG 	01 TCCATAACACTTGGGAAACT 	61 AACTGGACAACTACAAGAAA 	21 CAGAAGATGTGGAATAT 	81 ATCAAATAGTGGAAAG 	41 ACTACTATTGCAAATGGCAG 	01 TCATTGCCAAAAAGTTTCAG 	61 CTACTCCCTTTAAGGACTGC 	21 AGCAACCATCTTACATTGGA 	81 GATTGAATTGGCTCGCTCAT 	1 TGGGTCTGGGTAAAACAATA 	

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gatctgcaggcacag	CGGCTAGTCACAAAA 	GTGCTAGACCATTTP	GGTTCAACTCCATC?	TTTGGTGCTGAGGAA 	GATATAGATGAAATC 	GTAGGGGATGAGTTC gtaggggatg	GATATTGAGTTGGAA gatattgagttggaa	CAACGGAGAAGGATA 	CCGAGGATGAGAAAC ccgaggatgagaaac	AGGAGCAGAAGATA] aggagcagaagatat	AAGCGTGGAAGACC7 aagcgtggaagacct	ATCAGGCGGTTTATC 	GTAGCTAGAGATGCT 	CTTGTACATAATGGA Cttgtacataatgga	GGAGGTAGACTTGGC 	GCAAAACTAGTCATC gcaaaactagtcatc	GATCCAGAAGAAAGC 	
cacagaat	ATATTTAT atatttat	AGAAGATG	TGCATACA tgcataca	TTTTGAAG tttgaag	AGGAAATG aggaaatg	CATTGACT cattgact	ATGAAGAT atgaagat	CAGAATCC 	ACATGCTC acatgctc	GACGCAGT gacgcagt	GGCCAAAA ggccaaaa	ATGCAGAG atgcagag	TAGATGCT tagatgct	TGGGTGAA tgggtgaa	AAAGAGCA aaagagca	AGGTGAAT aggtgaat	TTCCTTCA ttccttca	
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AGAAG 	CAGACT	CIGGI 	CAAAAA 	AAGAT aagat	CTAAAA ctaaaa	CTATC	TGAGG tgagg	.GGGAG(GCCTG	TrGrG ttgtg	TCAAAA tcaaaa	CACAT	GTAGC gtagc	ACAGG acagg	TCAGT 	AGTGAT, 	AAGGA aaggaa
TAACAC taacac	cccrg cccgtg	GCTTG ggcttg	GGCTT 	CTGATG ctgatg	NGAAAAATC Ngaaaaatc	CAGTTC cagttc	AAAGAA 	CTGAAA(ctgaaag	CAGAAT 	GGATTT ggattt	TGCAAT 	GAATA	ATGATA atgata	ACAAAG acaaag	CAGCCT	CTAC	CCTGG
CAGCTT 	ACAGAC acagac	CAAA(caaa	GATGAA(gatgaa	AAAATC aaaatc	4 = 4	rGAACC tgaacc	CAAAGA 	CCTTC	CATTAC	TGT	AAACA 	CAATGT caatgt	CCATGA 	TCATCA tcatca	ATATTO	CAGATA cagata	GTCAAA(gtcaaa
SATCT gatct	CAGCTA cagcta	GAAGC/ gaagce	AATAA aataa	CAGA 	GAAAATI gaaaata	CAG	rGTG tgtg	GAAGGG gaaggg	SATCA gatca	GAAAAATT gaaaaatt	CTCTAC 	SCAG cag	AAAA 	CATGA	ಲ <u>್</u> – ಲ್ಲ	GGACAG(ggacag(CCACAGG
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5160 5340 5400 5400 5460 5460 5640 5700 5700 5760 5880 5880 6120 6120 6180 6180 5160 0009 0909 agaggtctccttatggttcaagatctcccctaggacacagatctccatttgaacactcat AGAGGTCTCCTTATGGTTCAAGATCTCCCCTAGGACACAGATCTCCATTTGAACACTCAT CAGATCACAAAAGTACACCTGAACATACATGGAGTAGCCGGAAGACATAACAAAGACTGA cagatcacaaaagtacacctgaacatacatggagtagccggaagacataacaaagactga TGTGCTGCAAATGTTGTGGCACTTTTTTTTTAAGAAATGGAAGATGTTTACTTTTACAGG TITCICCTGITIGGAICAGITATAAIGCCTTITITAIGAAACAAACAAAAAA ACTTAAAAGACAGCCGGGGTCATTCAGATCACCGCTCCCATTCAGACCACAGGATACACT CAGATCACCGTTCCACTTCAGAATACAGCCATCATAAATCTTCGAGAGATTATAGATACC CATTITCTGGACCTTCTTTTAGCCATATACAGTAAACTAACACAGGTAATTGCCTTACAT GACTTGAAAGATATGGACTGGATATTCTATCAGTAGCAGTATTGTTACTTCTTTCCAGGA TTCTAGGCTGAACACACAGATTAAATTATGTTTGTAAATGAACACTTAAAACACTGACCTGTG AAGGACTTTGTTCACTTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCC GCTTTTCATCACAAGCTTGAATATTTAAATTCTGTACCTACAGTTGTAAAATAGCCAGGA TCTTTTCACAAAGTCAGTATACTTACATGTTTTAATAAAATATCTCGATGGAATCAGAAT tcttttcacaaagtcagtatacttacatgttttaataaaatatctcgatggaatcagaat GTAAAAATGGGGAAGGGAATATTTTATTCCATTTAGTGCTCCTTTTTTATTGGATACTTT 5701 5281 5461 5521 5641 5101 5101 5161 5161 5221 5221 5281 5341 5341 5401 5401 5461 5521 5581 5581 5641 5701 5761 5761 5821 5821 5881 5881 5941 6001 6001 6061 6061 6121 6121 6181 g QQ g qq g QQ g qq g 셤 δy Db g Qλ ò QΥ δ g g qq οχ QQ qq q ò Ω Óλ Ω οy οy ο ò Ω Ω ò ò ó

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6301 TGATTGTTGTAATGAACAGTGAGAATATCCCACTCTAAACTGTGCCCTGGAAAGCTTTTC 6360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-IA gene (AAT42751) is suggested to initiate female development in birds. The sequence of CHD-W was deduced from 2 clones isolated from an 10-day chick embryo library using a fragment of the CHD-IA gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-IA give a W chromosome-specific signal on hybridisation to genomic DNA of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken CHD-W gene (partial sequence).
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                                                                                                             DB 18; Length 1316;
non-rarite bird and can be used for sex determin. of a bird. CH nucleic acids can also be used to control the sex of progeny of
                                                                                                         Query Match 16.6%; Score 1098.2; DB 18; Length Best Local Similarity 90.1%; Pred. No. 3.4e-29; Matches 1172; Conservative 0; Mismatches 129; Indels
                                                            Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
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The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or genes from Drosophila and for elucidating cell signalling and cell
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                    CCTTCAGATCCAGAAGAAAGGAAAAGATATGTCATCCCATGCCACCAAGGCTGCTCAC
                                                             TTCGATATAGATTGGGGTAAAGAAGATGATTCCAATCTGTTAGTAGGCATCTATGAATAT
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                                                                                                                                                                                                                                                                                                                                                                   NO 13811.
                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTTTG-----AAAAGTCAAAGGAGCTGGGAGAAATACAGTATCTTATTAAATGG
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                                                                     Sequence 6240 BP; 1675 A; 1682 C; 1760 G; 1123
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specification, but was obtained in electron:
at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                          Score 867.4;
Pred. No. 1.1
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Best Local Similarity 55.0%;
Matches 2134; Conservative
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Oy Dp	3042	ACGACAGGAAAAACTGTTCTGCATACAGGTTCAACTCCATCAAGGTCTACACCT 3095
δō	6	CACCTATTTGAAGTTTCGTGCTGAGGAACTCTTTAAAGAA 315
oy Oy	3156	aggacgatetttegetateetgaa GAGAAGAACAGGAGCCCCAGGAAAT
qq	3196	
οy	3216	C
QQ	3254	gagaccogcaacgaagatccggaaatgccagcagcagacgacttgttgtccgccttcaaagtg 3313
oy op	3255	GATGACTTCCAAGTTCAAGGTGGCGAACTTTTCCAATATGGATGAAGATGATAT 3314
δy	3315	GAGTIGGAACCAGAAAGAAATICAAGAAATIGGGAAGAAATCATCCCAGAATCCCAACGG 3374
Dp	3374	
δλ	3375	AGAAGGATAGAGGAGGAAGAAGAACATGAAGAAATATACATGCTCCCGAGG 3434
Dp	3434	: 8
δλ	m	GAAACTGFGCAAAACAGATCAGCTTTAATGGGAGTGAAGGAAGCAGCAGTAGGAG-349.
QQ	3494	ggaaaactgccgctaaccaaaacgaagggáagcgtggagctggc
δŽ	3494	SATATICIGGATCIGATAGIGACICCAICACAGAA 3533
qq	3554	actoggattacgagetg
Οy	3534	AGAAAACGCCCAAAAAAGCGTGGAAGACCTCGAACCATTCCTCGAGAAAATATTAAAGGA 3593
QD	3614	ggacgacctcgcaagcgcgggcggccgaccatgaaggagaagatcaccg
δλ	3594	5:
QQ	3674	- O
δŏ	3654	GAAAGGTTAGATGCTGTAGACTAGAGATGCTGAACTGGTTGATAAATCTGAGACAGAC
qq	3734	caccgcatggaggccatcgcatgtgatgctgagctgcaggaaaagccactggcggaactg 3793
δλ	3714	TTAAAG
QQ	3794	aagegeeteggaagaatgetgeatgaeegetgegtteagtteetgeaegageaeaaggag 3853
οy	3774	GGACAAGAAAGAGGAGGTAGACTTGGGAAAGTTAAAGGCCCAACGTTTCGAA 3828
qq	3854	ı i aagagagtaagactgeg
δ	3829	TCTCAGGAGTGCAGGTGAATGCAAAACTAGTCATCTCTCA
g	3914	gocacettetecgttaagetggggggggteteetttaatgecaaaaagetgetggetgg 3973
٥y	3870	aagaagagctggcaccactgcacaaatccattccttcagatccagaagaaaggaaag
QQ	3974	
οy	3930	ATCCCATGCCACCCAAGGCTGCTCCATTTGGATATAGATTGGGGTAAAGAAG
qq	4034	tggagcttcaatatcaagacacgccccggtcttcgacgtggattggggcatcgagggg 4093
Οy	99	TTCCAATCTGTAGTAGGCATCTATGAATATGGCTATGGCAGCTGGGAAATGATAAA 404:
QQ	6	ycatttaccagtacggcattggatcctgggagcagatgaag 415
οy	4050	ATGGATCCAGATCTCAGCTTAACACAGAAGATTTTACCTGATGATCCAGACAGA

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                                                                                                                                                       ACCACACCCTCAGAAA----AATCTGATGAAGATGATGAGGAGGAGGATAACAAGGTA 4343
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                                                                                                                                                                                                                               ATAAAACAGTGGAAGAAAAATTTGTGGATTTTTGTGTCCAAGTTTACAGAATTTGATGCC
                                                                                        gacgetgetggcgacgeacgeaccgtcgccgaaagcagtaacagtcaagtagatecatet
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                        CAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAATAAAGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 13808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                     4704 AGAAAGCTGCACAAACTCTACAAACATGCAATCAAAAAG 4742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster.
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and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA (ABB57737-ABB72072).
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                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                 detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9933 BP; 2711 A; 2468 C; 2538 G; 2216 T; 0 other;
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Best Local Similarity 55.0%;
Matches 2134; Conservative
23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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92 GAATATCTGAAGTATCGCCAGTTTCCTTCCAGAGACTTGATGGATCAATAAAAGGGAA 	42 TTGAGGAAGCAAGTGGATCATTTCAATĠCAGAAGGATCAGAGGATTTCTGTTTTTA 	02 CTGTCTACAAGAGCTGGAGGATTAGGTATTACTTGGCATCTGCTGACACTGTAGTTATT	62 TITGATICIGACIGGAATCCACAGAATGATCIGCAGGCACAGGCGAGAGCTCATAGAATT	22 GGACAGAAGAACAGGTTAATATTATCGGCTAGTCACAAAGGATCAGTAGAAGAAGAT 	:TTGAAAGAGCCAAGAAGAAGATGGTGCTAGACCA 	42 ACGACAGGAAAAACTGTTCTGCATACAGGTTCAACTCCATCAAGCTCTACACCT	ATAAAGAAGAGT acaaggacgatc	ATAGATGAAAT attgatgaaat	16 GAAACTCGGGAAAATGAGCCAGGTCCATTGACTG	GTTCAAGGTGGCGAACTTTTCCAATATGGA .cgaagaggaaccgagcgattcggttagcaa	rGGAACCAGAAAGAAATTCAAGAAATTGGGAAGAA 	75 AGAAGGATAGAGGAGGAAAAGACAAAAAGAACTTGAAGAAATATACATGCTCCCGAGG 	TGCAAA cgctaa	CAGAAGATATTCTGGATCTGA 	AGAAAACGCCCAAAAAAGCGTGGAAGACCTCGAACCATTCCTCGAGAAATATTAAAGG	GTGATGCAGAGATCAGGCGGTTTATC 	CTAGAGATGCTGAACTGGTTGATAAATCTGAG
268	531	280	286	292	296	304	309	315	321	325	333	337	343	349	1 2	359	365
Oy Db	Qy Db	Qy Dp	Qy Db	Oy Dp	QY	Qy	Qy	Oy Op	Oy Dp	QY	Oy Dp	Qy Db	QY Dp	Oy Dp	Oy Db	Qy	Qy Dp

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3714 AGACGTTTGGGTGAACTTGTACATAATGGATGCATTAAGGCTTTAAAGGACAATTCATCT 3773
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                                                                                                                                                                               -TCTCAGGAGTGCAGGTGAATGCAAAACTAGTCATCTCTCAC
                                                                                                                                                                                                                                                                                               6454 gccaccttctccgttaagctgggtggcgtctcctttaatgccaaaaagctgctggcctgc
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                                                                                                                   3774 GGACAAGAAAGAGCAGGAGGTAGACTTGGGAAAGTTAAAGGCCCAACGTTTCGAA----
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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The can gene mapping are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving cornection and polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and animo acid sequences. AAS6419-AAS94564 represent novel human DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WIPO
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from WIP
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                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #21771.
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80.3%; Pred. No. 2.5e-110;
tive 0; Mismatches 158;
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 21771; 103pp; English.
                                                                                                              BP
                                                                                                          AAS85967 standard; cDNA; 4222
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2000US-0649167.
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Matches 662; Conserv
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                         1163 AATACAGTATCTTATTAAATGGAAAGGCTGGTCACACATCCATAACACTTGGGAAACTGA 1222
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3710 AGATCTAAGTCAAAAAATGGAAAGATTCTTGGACAAAAAAAGAGACAGATGGATTCA 3651
                                                                                        867 TC----AGAGGAGGAGGAGGATGATGATGATTATGATAAGAGAGGATCTCGTCGCCCA 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene expression product; diagnosis; tumour; colon cancer; colorectal adenocarcinoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia; hyperplasia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human colon cancer cell line SW480 cDNA clone SEQ ID NO:553.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2930 ATGTAAAGAAAGAATGAGGCCTGTTAAAAGCAGCTTTGAAACAAC 2887
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AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (Colon cancer) Cell line SWA80. The cDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2155 TGCAAAATTCCCTCAAAGAGCTGTGGTCTTTGTTGCATTCATCATGCCAGAAAATTTT 2214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2035 TCAATTGGGCATTCATAGGAGTTGATGAAGCTCATCGTTTAAAAAAATGATGACTCTTTC 2094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2275 TTCACAAAGAGCTTGAACCATTTTTACTAAGAAGAGTTAAAAAAAGATGTAGAAAAGTCTT 2334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2335 TACCTGCTAAGGTTGAACAAATTCTGAGGATGGAAATGAGTGCATTGCAGAAGCAATATT 2394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 TACAGAATTCCCTCAAAGAGCTCTGGTCTTTGCTACATTTCCATTATGCCAGAAAGTTTT 240
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Carroll E, Catino TJ, Derti A, Ford DM, Lewis ME, Monahan JE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.9%; Score 321.4; DB 21; Length 575; Similarity 95.4%; Pred No. 3.3e-60; Scorevative 0; Mismatches 61; Indels 0; 8; Conservative 0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 575 BP; 187 A; 109 C; 95 G; 181 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 350; 469pp; English.
                                                                                                  98US-0088801.
                                                           99WO-IB01062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dysplasia or hyperplasia.
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                                                                                                                                           (FARB ) BAYER CORP
                                                           09-JUN-1999;
                                                                                                  10-JUN-1998;
                                                                                                                                                                                                                            Schlegel R;
                   16-DEC-1999
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AAIS8444 standard; cDNA; 6475

AAI58444;

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us-08-973-363-10.rng

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2463 ttggetgatgatgagatgggeettgggaaaaetgtacagacagcagtetteetgtatteeett 2522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the encoded polypeptides (AAAM36842-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemoteactic/chemokinetic activity, hemoteactic/chemokinetic activity, hemoteactic/chemokinetic activity, day screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang D;
                                                            cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1668 TATCAGTTAAATGGATTGAATTGGCTCGCTCATTCATGGTGCAAAGGAAATAGTTGTATT 1727
                                                                    peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; hardington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for treating disorders
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Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6475;
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.7%; Score 311.2; DB 22;
53.5%; Pred. No. 1.5e-57;
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tu C, Xue AJ,
Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides, us
system injuries
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                                                           immunosuppressant;
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                                  polynucleotide SEQ ID NO 647.
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Wehrman T, Xu
Goodrich R,
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2000US-0552317.
2000US-0598042.
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2000US-0653450.
2000US-0662191.
2000US-0693036.
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           (first entry)
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Wang Z,
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C.N.S disorders
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                      leukaemia; ss
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09-JUL-2000;
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          22-OCT-2001
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gaaggttataaaatacgaacgcatcgatggtggaatcactgggaacatgcggcaagaggcc 3542
TTTCATGAACATCAACTGTATGGCCCTTTTCTTCTGCGCGTGCCACTTTCTACCTTGACA
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                                                                                                                                                      1848 TCTTGGCAAAGAGAGATTCAAACTTGGGCTCCTCAGATGAATGCTGTAGTTTACTTAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ACGATTAAAGTTTAACATACTT
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The present sequence encodes a 218 kD dermatomyositis specific autoantique, designated Mi-2. The sequence numbering given in the specification starts at nucleotide 91, i.e. the 5' UTR is omitted, as well as the 'A' of the first ATG start codon. The protein is hydrophilic, acidic and protruding regions of the protein are characteristic of helicases. The gene corresponding to this cDNA was localised to chromosome I2 (12pl3). The DNA can be used for the recombinant production of Mi-2 which is used for .e.g. the differential diagnosis of collagen diseases, esp. dermatomyositis, e.g. by immunoassay or Mestern blotting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= Mi-2
/note= "the first ATG is at nucleotide 90, the sequence
given starts at nucleotide 91"
1579..6417
2817 GGAGGATTAGGTATTAACTTGGCATCTGCTGACACTGTAGTTATTTTTGATTCTGACTGG 2876
                                   3603 gggggccttggaatcaatctggccactgctgacacagttattatctatgactctgactgg 3662
                                                                   2877 AATCCACAGAATGATCTGCAGGCACAGGCGAGAGCTCATAGAATTGGACAGAAGAAACAG 2936
                                                                                                       3663 aacccccataatgacattcaggcctttagcagagctcaccggattgggcaaaataaaaag 3722
                                                                                                                                           2937 GITAATATITTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATGTTGTTGAAAGAGCC 2996
                                                                                                                                                                             3723 gtaatgatctaccggtttgtgacccgtgcgtcagtggaggaggagcgcatcacgcaggtggca 3782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding dermatomyositis specific auto:antigen - useful for differential diagnosis and treatment of dermatomyositis
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dermatomyositis specific autoantigen, Mi-2, coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mi-2; autoantigen; collagen disease; chromosome 12; 12p13; helicase; dermatomyositis; diagnosis; ss.
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                                                                                                                                                                                                               2997 AAGAAGAAGATGGTGCTAGACCATTTAGTAATTCAG 3032
                                                                                                                                                                                                                                                   3783 aagaagaaaatgatgctgacgcatctagtggtgcgg 3818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        AAT32301 standard; cDNA; 6327 BP.
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6234..6240
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2184 tatcaaatggagggcctgaattggttgcgcttctcctgggctcagggcactgacaccatc 2243
                                                                                                                                                                                                                                                                            1788 ITTCATGAACATCAACTGTATGGCCCTTTTCTTCTGCGCGGTGCCACTTTCTACCTTGACA 1847
                                                                                                                                                                                                                                                                                                                                                               2304 tacaaggagggtcattccaaaggccccttctagtgagcgccctctttctaccatcatc 2363
                                                                                                                                                                                                                                                                                                                                                                                                                        1848 TCTTGGCAAAGAGAGATTCAAACTTGGGCTCCTCAGATGAATGCTGTAGTTTACTTAGGA 1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1908 GATATAACTAGTAGAAATATGATAAGGACTCATGAATGGATGCATCCACAGACTAA---- 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2424 gacaaggacagccgtgccatcatccgagagagtgagttctcctttgaagacaatgccatt 2483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1964 ----ACGATTAAAGTTTAACATACTT 1985
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                                                                                                                                                                                                                                                     1668 TATCAGTTAAATGGATTGAATTGGCTCGCTCATTCATGGTGCAAAGGAAATAGTTGTATT 1727
                                                                           Ouery Match 4.7%; Score 309.6; DB 17; Length 6327; Best Local Similarity 53.4%; Pred. No. 3.2e-57; Matches 756; Conservative 0; Mismatches 609; Indels 51;
                 Sequence 6327 BP; 1761 A; 1473 C; 1740 G; 1353 T; 0 other;
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         3144 tctgggaaattattgctgctgcagaaaatgctcaagaaccttaaggagggtgggcatcgt 3203
                                                                              3443
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                                                                                                                                                                                                                                                                                                                                                                                                                     PKL; chromo domain; helicase domain; DNA binding domain; CHD3 protein; zinc finger domain; transgenic plant; chromatin remodelling factor; LEC1; pickle root; developmental identity; embryo development; ss.
                                                                                                                                                  GGAGGATTAGGTATTAACTTGGCATCTGCTGACACTGTAGTTATTTTTGATTCTGACTGG 2876
                                                                                                                                                                                         AATCCACAGAATGATCTGCAGGCACAGGCCGAGAGCTCATAGAATTGGACAGAAGAAACAG 2936
                                                                                                                                                                                                                                 GTTAATATTTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCC 2996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/note= "Encodes zinc finger domain; this region is
specifically referred in claim 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Encodes DNA binding domain; this region is specifically referred in claim 4"
                                                3204 gtactcatctttcccagatgaccaagatgctagacctgctagaggatttcttggaacat
                                                                   3384 gggggccttggaatcaatctggccactgctgacacagttattatctatgactctgactgg
                                                                                                                                                                                                      CIGGATCATITCAAIGCACAGGAICAGAGGAITICIGITTTTACIGICIACAAGAGCI
                             GTTCTGATTTTCTCTCAGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           this region 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343..453
/*tag= c
/*ote= "Encodes chromo domain -I; this region 571..681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= e
/note= "Encodes helicase domain; this region
specifically referred in claim 4"
3205..3285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "Arabidopsis thaliana PKL protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /uoce= "Encodes chromo domain -II;
is specifically referred in claim 6
877...2217
                                                                                                                                                                                                                                                                       AAGAAGAAGATGGTGCTAGACCATTTAGTAATTCAG 3032
                                                                                                                                                                                                                                                                                         3564 aagaagaaaatgatgctgacgcatctagtggtgcgg 3599
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          AAD02817 standard; cDNA; 4177 BP
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/note= "Encodes
                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana PKL cDNA.
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The invention relates to a method of regulating plant developmental identity which involves transforming a host cell with a nucleic acid encoding PKL (plckle) protein having atleast one chromo domain, a helicase domain, a DNA binding domain and a zinc finger domain.

This method is useful for transforming a host cell with PKL proteins for regulating developmental identity, such as for regulating the proteins act as chromatin remodelling factors to repress transcription of LEC1, a protein that plays a role in regulating embryo development. The proteins also used for generating transgenic plants expressing PKL proteins.

The present sequence is a cDNA coding for Arabidopsis thaliana PKL protein found in pickle root. PKL functions in regulating developmental dentity in host cells. It is classified as CHD3 protein based on the presence of chromo domain, SNR2-related helicase/ATPase domain, CNA-binding domain and PHD zinc finger domain.
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|1230 tctaaaaccaattaagtgggagtgcatgattgtgtgatgaaggtcatcgactgaaaaataa 1289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell with a nucleic acid encoding a PKL protein having at least one chromo domain, a helicase domain and a DNA binding domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Regulating plant developmental identity comprises transforming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
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55.6%; Pred. No. 1.9e-54;
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                                                                                                                                                                                                                       99US-0149975
                                                                                                                                                  18-AUG-2000; 2000WO-US22725
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Matches 635; Conservative
                                                                                                                                                                                                                                                                                                 (PURD ) PURDUE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                          Somerville CR;
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WO200114519-A2
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2501 TTGCTACCTCATTAAGCCACCAGATGATGAATTCTATAATAAAACAGGAGGCCTTACA 2560
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                                                                                                                                                                                                                                                                                                                                     2621 AGAACGTGGCAACAGAGTTCTGATTTTCTCTCAGATGGTGAGGATGCTGGACATCCTAGC 2680
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                                                                                                                                   2441 AAAAGGCAGTACCTCAGGCTTTCTGAACATTATGATGGAACTTAAGAAGTGTTGTAACCA 2500
                                                                                                                                                                                                                                     tccttatatgctagag---ggtgttgagccagttattcacgacgcaaatgaagctttcaa 1763
                                                                                                                                                                                                                                                                    2561 GCATTTGATACGTAGCAGCGGGAAACTAATCCTTGACAAGCTACTGATTCGTCTGCG 2620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1944 tgagcggcaaatacgcatagatcggttcaatgccaaaaattctaacaagttttgtttttt 2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTGATTCTGACTGGAATCCACAGAATGATCTGCAGGCACAGGCGAGAGCTCATAGAAT 2920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridastion probes, polypeptide (II) sequences. (I) is useful as hybridastion probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving a polypeptide in itssue, as molecular weight markers and as food supplement. (II) and its binding partners are useful for treating a food supplement. (II) and its binding partners are useful for treating clisorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics. formsics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of date and products dependent on DNA and diagnostic coding sequences of the invention.

Whose: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1648 AAAGICTGGAGTTAAGAGATTAICAGTTAAATGGATTGAATTGGCTCGCTCATTCATGGT 1707
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Matches 765; Conservative 0; Mismatches 623; Indels 57; Gaps
                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic alsorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.1%; Score 274.2; DB 23; Length 3031;
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 9710; 103pp; English.
                                                                                                                                               Tang YT;
                    31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                       WPI; 2001-639362/73.
P-PSDB; ABG09719.
                                                                                                                                               Drmanac RT, Liu C,
                                                                                              (HYSE-) HYSEQ INC
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                           TAGGAGTTGATGAAGCTCATCGTTTAAAAAATGATGACTCTCTTCTGTACAGGACTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                    SEQ ID NO 14027
                                                                                                             developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23; Length 8112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 14027; 21pp + Sequence Listing; English.
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Pred. No. 7.5e-4
0; Mismatches (
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 BP
ABL06515 standard; cDNA; 8112
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                                                       (first entry)
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Best Local Similarity 52.65
Matches 757; Conservative
                                                                                                                             pharmaceutical; gene; ss.
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                                                                                                                                                     Drosophila melanogaster.
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P-PSDB; ABB62412.
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interactions
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical; gene; ss.
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P-PSDB; ABB70172.
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cgaacacctgcctgggtgacgatgcattgattacgcgtttgcatgccgtgctgaaacctt 1340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotatic; chemotatic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.
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Wang J, Wang Z, Wehrman T, Xu C, Xue AJ,
Zhao QA, Zhou P, Goodrich R, Drmanac RT;
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25-APR-2000; 2000US-055317.
09-JUL-2000; 2000US-059042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653191.
19-OCT-2000; 2000US-063336.
29-NOV-2000; 2000US-0727344.
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Immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                        system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, ettivinibin activity, chemoteactic/chemokinetic activity, haemostatic and thrombolytic activity, carcer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 6553 BP; 1802 A; 1538 C; 1829 G; 1384 T; 0 other;
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Pred. No. 6.3e-42;
0; Mismatches 621; Indels
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52.1%;
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                       ----ATTAAGCCACAGATGATAATGAATTCTATAATAAACAGGAGGCCTTACAGCATT
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27-AUG-1999;
11-JAN-2000;
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09-JUN-2000;
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(HELI-) HELIX RES INST

418 tgactggcacccctctccaaaatacagttgaagaactatttagtcttcttcacttcttg 477

Yamamoto Saito K, , Otsuki' Isogai T, Nishikawa T, Hayashi K, S Sugiyama T, Wakamatsu A, Nagai K, Ishii S,

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length oDNAs.

Claim 8; SEQ ID 14295; 2537pp + CD ROM; English.

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the collgonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide comprises a fleast 15 nucleotides and the compination of the 5-end sequence/3-end sequence is selected from those defined in ctre specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length CDNAs. The primers are also useful for the detection and/or diagnosts of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the AMH18613 to AMH18613 represent human amino cold sequences; AMB3446 to AMH18613 to AMH18613 represent human amino cold sequences; AMB3446 to AMH18613 repr the present invention.

Sequence 2195 BP; 718 A; 391 C; 494 G; 592 T; 0 other;

; 9 1905 GGAGATATAACTAGTAGAAATATGATAAGGACTC----ATGAATGGATGCATCCACAGA 1959 2080 ATGATGACTCTTCTGTACAGGACTTTAATAGACTTTAAGTCCAACCATCGACTTCTGA 2139 1735 ATGAAATGGGTCTGGGTAAAACAATACAAACAATTTCTTTTCTGAACTACCTGTTTCATG 1794 1795 AACATCAACTGTATGGCCCTTTTCTTCTGCGCGTGCCACTTTCTACCTTGACATCTTGGC 1854 1855 AAAGAGAGATTCAAACTTGGGCTCCTCAGATGAATGCTGT------AGTTTACTTA 1904 1960 CTAAACGATTAAAGTTTAACATACTTCTGACGACATATGAAATTTTACTGAAGGATAAGT 2019 2020 CATICCTIGGIGGICICAATIGGGCAITCAFAGGAGTIGAAGAGCICAICGITTAAAA 2079 2140 TTACTGGAACCCCACTGCAAAATTCCCTCAAAGAGCTGTGGTCTTTGTTGCATTTCATCA 2199 58 tgactggtataagaggacctttcctgattattgctccactttctactattgcaaactggg 117 238 gaggagcttacagattccaagccatcatcacttttgaaatgattcttggaggctgtg 297 298 gagagcttaatgcaattgaatggaatgtgtgattattgatgaagcacataggttaaaaa 357 358 ataaaaaattgtaaactcttagagggcctgaaactcatgaatctggaacacaaggtgcttt 417 118 agagagaatttcgtacgtggactgatattaacgttgtggtttatcatgggagcctgatta 177 51; Gaps Score 236.6; DB 22; Length 2195; Pred. No. 1.7e-41; 0; Mismatches 609; Indels 3.6%; Best Local Similarity 51.9%; Matches 713; Conservative Query Match g Dp g ò q õ g ò à ò

2436 2587 TAATCCTTCTTGACAAGCTACTGATTCGTCTGCGAGAACGTGGCAACAGAGGTTCTGATTT 2646 2647 TCTCTCAGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTATCGCCAGTTTC 2706 2767 TCAATGCAGAAGGATCAGAGGATTTCTGTTTTTACTGTCTACAAGAGCTGGAGGATTAG 2826 GTATTAACTIGGCATCTGCTGACACTGTAGTTATTTTGATTCTGACTGGAATCCACAGA 2886 2887 ATGATCTGCAGGCACAGGCGAGAGCTCATAGAATTGGACAGAAAACAGATTAATATT 2946 2947 ATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAAGAAGAAGA 3006 1258 acagactggtaactcgtaactcatatgagagagatgtttgaccgagccagtttgaaac 1317 2200 TGCCAGAAAATTTTCCTCCTGGGAAGATTTTGAAGAGGAGCATGGCAAAGGAAGAGGAGT 2259 2260 ATGGTTATGCA---AGTCTTCACAAAGAGCTTGAACCATTTTTACTAAGAAGAGTTAAAA 2316 2317 AAGATGTAGAAAAGTCTTTACCTGCTAAGGTTGAACAAATTCTGAGGATGGAAATGAGTG 2376 2437 GTTCAAAAGGCAGTACCTCA---GGCTTTCTGAACATTATGATGGAACTTAAGAAGTGTT 2493 2494 GTAACCATTGCTACCTCATTAAGCCACCAGATGATAATGAATTCTATAATAAACAGGAGG 2553 538 aggaacaggtacagaaacttcaggttatcctgaaaccaatgatgttgagacgattaaaag 597 aagatgtggaaaagaagttggcacctaaagaagaaaccatcattgaagtagaacttacta 657 718 gagcaggacaaactaatgtacctaacttggtcaataccatgatggagctcaggaaatgtt 777 778 gtaatcatccatatcttataaaaggtgctgaggagaaaatacttggagaatttagagata 837 838 cttacaatccagctgcttctgattttcatcttcaagcaatgatccagtctgctggtaaat 897 478 aaccettaaggitteettetgaateaacaittatgeaagaattiggggatetgaaaacag 537 2377 CATTGCAGAAGCAATATTACAAGTGGATTTTAACAAGGAATTATAAAGCCCTCAGTAAAG 3007 TGGTGCTAGACCATTTAGTAATTCAGAGAATGGACACGACAGGAAAAACTGTT 3059 Q g q ŏ QQ δ g δý qq δ q ò g δy g δ g ò g δ g δ 셤 δ δλ

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6.2 G19 9 BB155356 BB155356 BB155356 BB155356 BB153356 BB155356 BB153356 BB153356 BB153356 BB153356 BB153356 BB153356 BB1533285 BB238285 BB2382828 BB238285 BB238285 BB2382828 BB23822828 BB23828288 BB23822828 BB23822828	ALIGNMENTS AKO15218 AKO15218 Ball bp mRNA linear HTC 19-JAN-2002 Mus musculus adult male testis cDNA, RIKEN full-length enriched 1. full insert sequence. AKO15218 AKO15218. AKO152	weth. Engymol. 303, 19-44 (1999) 99279253 10149636 2 (sites) 2 (sites) 2 (sites) CarnincI.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Ltoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 6enome Res. 10 (10), 1617-1630 (2000) 1049374 11042159 3 (sites) Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Suni,N., Ishi,Y., Mushi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishi,Y., Makamura,S., Hazama,M., Nishine,T., Harda,A., Yanamoto,R., Matcsuncto,H., Sakagucihi,S., Ikagami,T., Kashiwagi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., KIRKN integrated sequence analysis (RISA) system-584 format sequencing pipeline with 384 multicapillary sequencer
118 406.4 119 4 002.4 22 23 395.6 22 395.6 24 3995.6 25 379.6 26 379.6 27 376.6 28 379.6 29 376.6 31 31 310.6 41 3131.8 41 3131.8 45 3117.4 45 3114.6	π Ζ Σ	DOUNTAL MEDLINE MEDLINE D10349636 REFERENCE AUTHORS TITLE TITLE TOWN MEDLINE D1034036 REFERENCE TOWN MEDLINE TOWN MEDLINE MEDLINE TOWN MEDLINE MEDLINE TOWN MEDLI
4.5 Compugen Ltd. Compugen Ltd. Search time 8940.62 Seconds (without alignments) 9975.581 Million cell updates/sec 9975.581 Million cell updates/sec sidues ssidues sters: 27472414	results predicted by chance to have a lot the score of the result being printed, of the total score distribution.	Description AK015218 Mus muscu BM491730 pgp2n.pk0 BH657861 603282944 BM486590 pgm2n.pk0 BM475844 AGENCOURT AU11528 AU11728 AU125712 AU125712 AW957058 QV3-8N004 AW67566 he21e07.x BG538825 602568268 AK0118451 Mus muscu BE612384 601451944 AV72238 AV72238 A1226723 AG5505962 BR427718 df89611.y BG618563 602505962
nnCore version 4.5 1993 - 2000 Compugating sw model 12, 16:52:15; Search 9975. 10 CGAAGCGCAA sapext 1.0 6748477542 residues 9 chosen parameters: 100 08 45 summaries	EST:* 1: em_estba:* 2: em_esthum:* 3: em_esthum:* 4: em_estru:* 5: em_estor:* 6: em_estp:* 7: em_estro:* 8: em_estro:* 10: gb_estro:* 10: gb_estro:* 11: gb_htc:* 11: gb_htc:* 12: gb_estro:* 13: em_gss_hum:* 14: em_gss_hum:* 14: em_gss_hum:* 15: em_gss_hum:* 16: em_gss_hum:*	ID MACUIS 218 BMA91730 BMA91730 BMA957261 BMA957261 BMA75844 AULITS 28 AUU15712 AUU15712 AUU15712 AUU15712 AUU15756 AUU15756 AUU15757 BEG12384 AV779238 BEG12384 BEG136771

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RRLEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRSRSRRYSGSDSDSISERKRPK
KRGRPRTIPRENIKGFSDAEIRR"
  IQRMDTTGKTVLHTGSAPSSSTPFNKEELSAILKFGAEELFKEPEGEEQEPQEMDIDE
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                                                                                                                                                                                                                                                                   DB 11; Length 1811;
                                                                                                                                                                                                                                                                                     Pred. No. 1e-147;
0; Mismatches 251; Indels
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                                                                                                       /note="putative"
1811
                                                                                                                                                       /note="putative"
                                                                                                                                                                                                                                                                   17.3%;
83.8%;
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Best Local Similarity 83.8
Matches 1295; Conservative
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Nature 409, 685-690 (2001)
E 5 (bases 1 to 1811)
S dachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Hanagaki,T.,
Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
Hume,D., Imotani,K., Ishi,Y., Itoh,M., Izawa,M., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Koda,M., Koya,S.,
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,R., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Sakai,C., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
Tanaka,T., Tejima,Y., Toya,T., Yamamaka,I.,
Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
Haysshizaki,Y.
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//dxxref="d01:1285371"
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AEYIKRPOPPFGRLGOSIKGELEKQALDHFNARGSEDFCFLLSTRAGGLGINLASADY
VVIFDSDWNPONDLOAQARAHRIGGKKQVNIYRLVTKGSVEEDILERRAKKWVLDHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="chromodomain helicase DNA binding protein 1 data source:MGD, source key:MGI:888393, evidence:ISS
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128. .1549
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/gene="Chd1"
                                                                                    FANTOM Consortium.
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AUTHORS
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JOURNAL
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2372

2432

2492

421

2672

841

541

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EST 12-SEP-2001
                                          /organism="Gallus gallus"
/organism="Commercial broiler chickens"
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/db_xref="taxon:9031"
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/clone=Inp="Normalized Chicken
/clone=Inp="normalized Chicken
/clone=Inp="normalized Chicken
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                                                                                                                                                                                                                                      /lab_host="F. coli EMDH10B"
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/hote="'vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue at different
pools of total RNA isolated from 5'-end"
ages Single pass sequencing from 5'-end"
ages 116 c 127 g 190 t . 12 others
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                                                                                                                                                                                                                                                                                                                                                                                  9.5%; Score 629.6; DB 10; Length 648; 97.5%; Pred. No. Se-77; ative 0; Mismatches 16; Indels 0;
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cogburn@udel.edu, www.chickest.udel.edu
Location/Qualifiers
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Gallus gallus

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Brasianidae; Gallus.

Ers from Normalized Chicken Pituitary/Hypothalamus/Pineal CDNA

Inhabilished (2002)

Contact: Larry A. Coghurn

University of Delaware

Townsend Hall, Newark, DE 19717, USA

Tel: 302-831-2822

Fax: 302-831-2822
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BM491730.1 GI:18612661
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1322 GAGAGACAAAAAGGAACTGGAGGAATTTATATGCTCCCGAGAATGAGAAACTGTGCAAAG 1381
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                                                                                                                                                         3033 AGAATGGACACGACAGGAAAAACTGTTCTGCATACAGGTTCAACTCCATCAAGGTGTACA 3092
                                                                                                                                                                                    GAAGAAGATATTCTTGAAAGACCCAAGAAGAAGATGGTGCTAGACCATTTAGTAATTCAG 3032
                                                                                                        ACCESSION
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SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2,
                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 888)
NIH-WGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
603282944F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5327267 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2020 CATTCCTTGGTGGTCTCAATTGGGCATTCATAGGAGTTGATGAAGCTCATCGTTTAAAAA 2079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCCAGAAAAATTTTCCTCCTGGGAAGATTTTGAAGAGGAGCATGGCAAAGGAAGAGAGT 2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2260 ATGGTTATGCAAGTCTTCACAAAGAGCTTGAACCATTTTTACTAAGAAGAGTTAAAAAAG 2319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Context: Robert Strausberg, Ph.D.
Email: ggapbs -r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM11830 row; g column: 12
Plate: LLAM11830 row; g column: 12
High quality sequence stop: 741.
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82.8%; Pred. No. 1.9e-70;
tive 0; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="Inbage:5327267"
/clone_lib="NIH_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
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EST 07-FEB-2002
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
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/clone_lib="Normalized Chicken Breast Muscle, Leg Muscland Elphyseal Growth Plate CDNA library (pgm2n)"
/sex="Male and Female"
/tissue_type="Breast muscle, leg muscle and epiphyseal
                                                                                                                                                                                       2500 ATTGCTACCTCATTAAGCCACCAGATGATAATGAATTCTATAATAAACAGGAGGCCTTAC 2559
                                                                                                                                                                                                                                                                                       2560 AGCATTIGATACGTAGCAGCGGGAAACTAATCCTTCTTGACAAGCTACTGATTCGTCTGC 2619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2739 GAATTGAGGAAGCAAGCACTGGATCATTTCAATGCAGAAGGATCAGAGGATTTCTGTTTT 2798
                                                                                                                      602 GAGAAACGAGGCAACCGAGTGCTCATTTTCTCTCAGATGGTGCGGATGTTAGACATACTC 661
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2380 TGCAGAAGCAATATTACAAGTGGATTTTAACAAGGAATTATAAAAGCCCTCAGTAAAGGTT
                           2620 GAG-AACGTGGCAACAGAGTTCTGTGATTTCTCTCAGATGGTGAGGATGCTGGACATCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2440 CAAAAGGCAGTACCTCAGGCTTTCTGAACATTATGATGGAACTTAAGAAGTGTTGTAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1679 GCAGAATATCTGAAGTATCGCCAGTTTCCCTTCCAGAGACTTGATGGATCAATAAAAGGG
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Cogburn, L.A. and Monsonego-Ornan, E.
ESTS from Normalized Chicken Breast Muscle, Leg Muscle,
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal
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Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Fax: 302-831-1335
Fax: 302-831-2822
Email: cogburnéudel edu, www.chickest.udel.edu.
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/strain="Commercial broiler and
Strains 90 & 21"
/db_xref="taxon:9031"
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Page 5

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/note-"Organ: eye; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."
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               Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
ficund through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMA1237 row b column: 06
High quality sequence stop: 650.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.2%; Score 473.6; DB 10; Length 1042;
75.7%; Pred. No. 9e-56;
tive 0; Mismatches 194; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                    /clone="IMAGE:5579813"
/clone_lib="NIH_MGC_67"
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                                                      /note-"Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth ptota 53.3% of the final RNA pool). Single pass sequencing from 5'-end"
/dev_stage="Breast_leg:Embryo(d19):post-hatch(1d,1,3,5,7,9,11ab_host="Ec. coli EmbH)08"
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1 (bases 1 to 1042)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5172 TCCACTTCAGAATACAGCCATCATAAATCTTCGAGAGATTATAGATACCACTCAGACTGG 5231
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 899)
Ota T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
153-2 Yana, Kiszarzu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Wirlology, Institute of Medical Science, University of Tokyo, and
                           1152
                                                                            1211 TTGGGAAACTGAAGAAACGC----TGAAGCAACAAAATGTTAAAGGAATGAACAAACTGG 1266
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                                                                                                                                                                                   1267 ACAACT - ACAAGAAAAAGGATCAGGAGACAAAACGCTGGCTGAAAAATGCTTCTCCAGA 1324
                       600 AAACCATAGAAAGATTTATGGATTGTCGGATTGGGAGAAAGGAGCTACTGGTGCTACTA 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU117528 AU17528 HEMBAl Homo sapiens CDNA clone HEMBAl001604 5', mRNA
                                                                                                                                                                                                  Length 899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/note="Vector: pME18SFL3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1001604"
/clone_lib="HEMBA1"
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Location/Qualifiers
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 866)
Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2876 GAATCCACAGAATGATCTGCAGGCACAGGCGAGAGCTCATAGAATTGGACAGAAGAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2336 ACCTGCTAAGGTTGAACAAATTCTGAGGATGGAAATGAGTGCATTGCAGAAGCAATATTA
                          2456 AGGCTTTCTGAACATTATGATGGAACTTAAGAAGTGTTGTAACCATTGCTACCTCATTAA
                                                                                                                                                                                                                                 2516 GCCACCAGATGATAATGAATTCTATAATAAACAGGAGGCCTTACAGCATTTGATACGTAG
                                                                                                                                                                                                                                                                                                                                                                                                          2576 CAGCGGGAAACTAATCCTTCTTGACAAGCTACTGATTCGTCTGCGAGAACGTGGCAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2816 TGGAGGATTAGGTATTAACTTGGCATCTGCTGACACTGTAGTTATTTTTGATTCTGACTG
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                                                                                                  2396 CAAGTGGATTTTAACAAGGAATTATAAAGCCCTCAGTAAAGGTTCAAAAGGCAGTACCTC
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AU125712 NT2RM4 Homo sapiens cDNA clone NT2RM4002061
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AU125712.1 GI:10950428
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HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sigano,S., Isogai,T.)
                                                                                                                                                                                                                                                                    Tel: 81-438-52-3951
Email: 94-38-52-3952
Email: 94-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3631 ACAAGAAATTTGGTGGCCCTCTGGAAAGGTTAGATGCTGTAGCTAGAGATGCTGAACTGG 3690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3691 TTGATAAATCTGAGACAGACCTTAGACGTTGGGTGAACTTGTACATAATGGATGCATTA 3750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3931 ATGTCATCCCATGCCACACCAAGGCTGCTCCATTCGATATAGATTGGGGTAAAGAAGATG 3990
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                                                                                                                                  Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 456.6; DB 9;
Pred. No. 2.1e-53;
0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pME185FL3; mR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NT2RM4"
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Best Local Similarity 81.5%;
Matches 568; Conservative
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/ub.-rel-_carul._soc./
/clone_lbb=RN0047.
/dev_stage="Adult"
/note="Organ: Dresst_normal; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A min!-library was made by choing products
derived from RORESTES POR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
lissue mRNA and cDNA amplification were performed under
low stringency conditions.
a 154 c 126 g 241 t
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Email: asimpsor@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtmil2.pl?tl=&t2=QV3-BN0047-150

Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                   AW997058 686 bp mRNA linear EST 05-JUN-2000
QV3-BN0047-150400-152-c03 BN0047 Homo sapiens cDNA, mRNA sequence.
AW997058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 68 arcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Cancer Genetics
Ladwig Institute for Cancer Tessearch
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3522 TCCATCACAGAAAGAAACGGCCAAAAAGCGTGGAAGACCTCGAACCATTCCT-CGAGA 3580
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4231 ATAAGAAGAATAA---GATGAAGGCTTCAAAAATAAAAGAAGAAATAAAAGAGTGATTCTT 4287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                4288 CACCACACCCTCAGAAAATCTGATGAAGATGATGA 4324
                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 678.
Location/Qualifiers
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/clone_lib-"NCI_CGAP_CML1"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/AF
rearrangement positive, includes both chronic phase and
myeloid blast crisis"
/clone="IMAGE:2919684"
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ilarity 84.6%;
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Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs remail.nih.gov

Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,

Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The

Technologies, Inc. cDNA Library Arrayed by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Www.bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 380.
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WW467566 1 GI:7037672
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Catarrhini; Hominidae; Homo.
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 609)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                     GGACAATTCATCTGGACAAGAAAGGGCAGGAGGTAGACTTGGGAAAGTTAAAGGCCCAAC 3820
                                                                                                                                                                                                                                                                                   3821 GTTTCGAATCTCAGGAGTGCAGGTGAATGCAAAACTAGTCATCTCTCACGAAGAAGAGGCT 3880
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GAATATTAAAGGATTTAGTGATGCAGAAATTAGCCGTTTTATCAAGAGCTATAAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                         146 CCTCAGTCTAACACACAAGATTCTTCCAGATGATCCCGATAA-AAACCACAAGCAAAACA
                                                         386 ATTCCGAATATCAGGAGTACAGGTGAATGCCAACTAGTCATCTCCCATGAAGAATT
                                      3641 TGGTGCCCCTCTGGAAAGGTTAGATGCTGTAGCTAGAGATGCTGAACTGGTTGATAAATC
                                                                                                                    3701 TGAGACAGACCTTAGACGTTTGGGTGAACTTGTACATAATGGATGCATTAAGGCTTTAAA
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
/lnb.host="NotB" //lnb.host="NotB" //lnb.host="Organ: whole blood; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally, Primer: Oligo dT. Library constructed by Life Technologies." a 143 c 98 g 211 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3018 CATTTAGTAATTCAGAGAATGGACACGACAGGAAAACTGTTCTGCATACAGGTTCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 CCATCAAGTTCTACTCCTTTCAATAAAGAAGAGTTATCAGCCATTTTAAAGTTTGGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3198 GAAATCTTGAAGAGAGCTGAAACTCGGGAAAATGAGCCAGGTCCATTGACTGTAGGGGAT
                                                                                                                                                                                       Length 609
                                                                                                                                                                                         DB 9;
                                                                                                                                                                                       Score 449.2; DB 9
Pred. No. 2.6e-52;
0; Mismatches 93
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//Lone="Inace: 69200"
//clone="Inace: 69200"
//clone="Inace: 69200"
//clone="Inace: 69200"
//clone="Inace: 69200"
//lab_bost="PulloB (TI phage-resistant)"
//note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfl1 (ggccgcctcggcc); Site_2: Sfl1 (ggccatcdgcc); S' adaptor
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CRGCGCGCAFTGCCC3" and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGAGCGCGCATGCT(30)BN-3' (where B = A, C, C or G and N = A, C, G, Or T). Average Insert size 19
kb (range 0.5-4.0 kb): 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                  National Mistitutes of Health, Manmalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CLONG Library Preparation: CLONTECH Laboratories, Inc.
CLONG Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCABIST Tow: g column: 17
High quality sequence stop: 639.
Location/Qualifiers
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1 (bases 1 to 895)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished (1999)
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/db_xref="taxon:9606"
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Mus musculus 16 days embryo lung cDNA, RIKEN full-length enriched library, clone:8430430D21:chromodomain helicase DNA binding protein 1, full insert sequence.
AKO18451 GI:12858158
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Carrintoi, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Carrintoi, P., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1017-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mass musculus (strain:C57BL/6J) 16 days embryo lung cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:8430430D21.
2862 TTTGATTCTGACTGGAATCCACAGAATG--ATCTGCAGGCACA-GGCGAGAGCTCATAGA 2918
                                                                                                                                                                                                                                                                                                                              2919 ATT---GGACAGAAGAACAGGTTAATATTTATCGGCTAGTCACAAAAGGATCAGTAGAA 2975
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 68-6090 (2001)

Chases 1 to 1346)

Adachl, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,
Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,
Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F.,
                                                                                                             2807 TACAAGAGCTGGAGGATTAGGTATTAACTTGGCATCTGCTGACACTG-----TAGTTATT 2861
                                                                                                                                         Carninci, p. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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 5254 GTAGTGGCCCGAGGTCACCACTAGATCAGAGGTCTCCTTATGGTTCAAGATCTCCCCTAG 5313
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/protein_id="BaB31219.1"
/db_xref="G1:12858159"
/translation="RSSRDYRYLSDWQLDHRAASSGPRSPLDQRSPYGSRSPFEHSAE
                                                                                                                                                                                         Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
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/tissue_type="lung"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="16 days embryo"
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78 ACAAATCACGATGATAGCAGCAGGACAGTTATTCCTCTGATAGACACTTAACTCAGTAC 137
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/lab_host="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="bloot="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1100)
4839 ACAAACCATGATGATAGTAGCAGGGACAGTTATTCTTCTGATAGACATTATCACAATAC 4898
                                                                                                                                                                                                                                                                                                           4779 AGCAGCAATGTGAATACACATGTAATCAGAAATCCAGATGTGGAAAGACTGAAGGAGACT 4838
                                                                                                                  6358 TTCAGGTGCATTGGTTTAAAAGAAGGAAGTGTTCTATAGGTGAACACTTCAAAACCCAGA 6417
                                                                                                                                                                                             1111 CCCAGTGCATTGGGTTGAAAGGGTGGTAGGTGTATGAACACTTAAAATCCAAA----- 1163
                                                                                                                                                                                                                                                                        6418 TCAGCCAAGATTCATTGTAAATCCATTTGTTTTCCCTCTTTAACATGGGCAATAATGTCA 6477
                                                                                                                                                                                                                                                                                                                                                                                                                         6478 AATGTGCTATGCAGC---AGTTAATATTTAGAAGATTTGAATGACTTTATAACAGAAT 6534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
floud through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Best Local Similarity 75.7%; Pred. No. 4.3e-50;
Matches 639; Conservative 0; Mismatches 170; Indels 35; Gaps
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High quality sequence stop: 700.
Location/Qualifiers
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Context: Robert Strausberg, Ph.D.
Email: cgapbs-rémail nih gov
Tissue Procurement: DCTD/DTP
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_66"
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Eukaryota' Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliais Eukheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 804)

Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Ofan,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu, X., S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,Z., and Han,Z.

Homo sapiens cDNA HTC clones

npublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 17-OCT-2000
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                                                                                                   4959 AGGCCATATTCAGCCTTCAGTAATGGAAAAGATCACAGAGACTGGGATCACTACAAACAG 5018
                                                                                                                                                                                                 5076 GACCACAGGTCAAACCTGGAAGGAAACTTAAAAGACAGCCGGGGTCATTCAGATCACCGC 5135
                                                                                                                                                                                                                                                                                                                                                                                                            5136 TCCCATTCAGACCACAGGATACACTCAGATCACCGTTCCACTTCAGAATACAGCCATCAT 5195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5196 AAATCTTCGAGAGATTATAGATACCACTCAGACTGGCAAATGGACCACAGAGCTTCTGGT 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5256 AGTGGCCCGAGGTCACCACTAGATCAGAGGTCTCCTTATGGTTCAAGATCTCCCCTAGGA 5315
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4899 CATGATCATCACAAAGACAGGCATCAGGGAGATGCTTACAAGAAAGTGACTCCAGGAAA 4958
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                                                                                                                                                                                                                                                                                                                                                                                                                                    657 ATCATAAACCAACACAGTAATTGCCTTACATGACTTGAAAGATATAAACAGAATCTTCTA 716
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EST 23-DEC-1998 one IMAGE:582689

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1 (bases 1 to 808)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                          AI326723 808 bp mRNA linear EST 23-DEC-19
mq55h09.yl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:5826
5' similar to gb:L10410 Mouse DNA binding protein (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4599 GATCACATTACAGAATGCCTGAAGGAGTACACAAATCCCGAGCAAATAAAACAGTGGAGG 4658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:357337
654 TCACTACAAGCAAGACAGGATATACAGTGACAGAGAACCACAGAAACCTGATGATC 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                   Score 431.4; DB 9;
Pred. No. 6.1e-50;
0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MAMouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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/clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 454.
Location/Qualifiers
of /Organism="Mus musculus" / strain="C57BL/6J" / db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
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Matches 601; Conservative
                                                                                                                                                                                                                                                                                          house mouse.
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                                                                                                                                                                                                                                               /tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
             Chinese National Human Genome Center at Shanghai
201203. P. R. China
201203. P. R. China
1201203. P. R. Shangqengers, R. Shanghai.
1201203. P. China is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4406 TCATATTACTGCAACCAGTGAACCAGTTCCTATCTCAGAAGAATCTGAAGAACTCCATCA 4465
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0; Mismatches 172;
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                                                                                                                                                        1. :804
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTCBBH12"
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Email: cgapbs-remail.nih.gov

Tissue Procurement: CLOWTECH Laboratories, Inc.

CDNA Library Preparation: CLOWTECH Laboratories, Inc.

CDNA Library Preparation: CLOWTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://ingape.llnl.gov

Plate: LLCM1378 row: I column: 15

High quality sequence stop: 593.

I. 765

I. 765

I. 765

Arrayed by: The Sequence stop: 606*

/ Clone library ware used in cloning as follows: 5' adaptor sequence: 5' -AATCTAGAGGCAGGAGGCACAATG-GT(30)BN-3' (where B = A).

Crone and N = A, C, G, or T). Average insert sequence: 5' -AATCTAGAGGCAGGGGGCACAATG-GT(30)BN-3' (where B = B).

C, or G and N = A, C, G, or T). Average insert sequence: 5' -AATCTAGAGGCAGGGGGCGCAATTGGGCCAATGAGGCCGACAATGAGGCCGAATAATGGCC'' and 3' adaptor sequence: 5' -AATCTAGAGGCCGGGCGACAATGAGGCCGAATAATGGCC'' and 3' adaptor sequence: 5' -AATCTAGAGGCCGGGCGACAATGAGGCCGCAATTAGGCC'' and 3' adaptor sequence: 5' -AATCTAGAGGCCGGGCGACAATGAGGCCGCCAATTATGGCC'' and 3' adaptor sequence: 5' -AATCTAGAGGCCGGCGCCAATTATGGCC'' and 3' adaptor sequence: 5' -AATCTAGAGGCCGGCGCCAAATGAGGCCGCCAAATGAGGCCCGAAATGAGGCCCCAAATGAGGCCCGAAATGAGGCCCGAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCCCAAATGAGGCCC
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602505962Fl NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4619294 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 765)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                  4719 CTCTACAAACATGCAATCAAAAAGCGCCAAGAGTCTCAGCAACACAATGACCAAAACATT 4778
                                                                                                                                                                                                                                                                               1779 AGCAGCAATGTGAATACACATGTAATCAGAAATCCAGATGTGGAAAGACTGAAGGAGACT 4838
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                                   1;
Length 765;
6.4%; Score 422; DB 10; Length 7 ilarity 83.0%; Pred. No. 1.2e-48; Conservative 0; Mismatches 100; Indels
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541 AGCATTAACGGATAGTTCTTCAGGAACAGAACGAACAGGTGGTAAGACTCGGAA 594 QQ

Search completed: August 2, 2002, 16:53:13 Job time: 12274 sec

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AF6693 Sequence 12
AF004397 Gallus ga
AC01222 Homo sapi
AC012624 Homo sapi
AC021249 Homo sapi
AC021249 Homo sapi
AC021249 Homo sapi
AC021249 Homo sapi
AC02124 Homo sapi
AC02124 Homo sapi
AC022382 Homo sapi
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AC022852 Homo sapi
AX16599 Sequence 14
AX16599 Sequence AC0702852 Homo sapi
AX24659 Sequence
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Griffiths,R. and Thwarl,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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Other publication AU 5906996 961224.
Location/Qualifiers
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Sequence 12 from Patent WO9639505.
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A58693.1 GI:3714251
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/organism="unidentified"
/db_xref="taxon:32644"
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A58693
                                                                            August 2, 2002, 20:55:27; Search time 12674 Seconds (without alignments) 437.553 Million cell updates/sec
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                                                                                                                                                                                                                                                                                    265
1 GATGAGATTGTTTCAGTGAA......AAGAAGTGAAGGAAGAAGAAG 265
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                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                             1797656 seqs, 10463268293 residues
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Gapop 10.0 , Gapext 1.0
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 6872)
Griffiths, R. and Korn, R.M.
A CHPI gene is Z chromosome linked in the chicken Gallus domesticus Gene 197 (1-2), 225-229 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 6872)
Griffiths, R. and Korn, R.M.
Direct Submission
Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University,
Glasgow G12 800, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDDEDYDKRGSRRQATVNVSYKEAEETKTDSDDLLEVCGEDVPQTEEDEFETIEKFMD
SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
LKQQNVKGMNKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVBRII
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Gallus gallus chromo-helicase-DNA-binding on the Z chromosome
protein, variant with hydrophilic domain, (CHD-Z) mRNA, complete
                                                                                                                  61 AGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGAGACAAA 120
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/genet.
/function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
                           Indels
  Length
Score 265; DB 6;
Pred. No. 1.1e-27;
                           Mismatches
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/db_xref="taxon:9031"
11. .6872
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ELSTRAGGEGINIMASADTVIFDSDMVDQNDLOAQARAHRTGOKKOVNIYRLYRGS
VEEDILERAKKKMVLDALVIQRADTTGKTVLHTGSTPSSSTPFNKEELSAILKFGAEE
LFKEPEGEEQEPQEMDIDEILKRAETTRENEPGPLIVGDELLSQFKVANFSNMDEDDIE
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SRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLERLD
AVARDAELVDKSETDLRRLGELVHNGCIKALKDNSSGQERAGGRLGKVKGPTFRISGV
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REAGAGONSKRRKTRNKKNMKAASKI KEEI KSDSSPQPSEKSBEDBEEEDNKDEIVSVK
HILHKI IKTERENEERPEPDIGIKKEAEERFEKEREKREIKREKREKEREKIEKEK
NKEKRENKVKESTQKEKEVKERKVNEWKSENEKSKKI PLLOTPVHITATSEPVPISE
ESEELHQKTFSVCKERMRPVRAALKQLDRPEKGLSEREQLEHTRQCLIKIGDHITECL
                                             RTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYGYAS
LHKELEPFLLRRVKKDVEKSLPAKVEQILRMEMSALQKQYYKWILTRNYKALSKGSKG
STSGFLNIMMELKKCCNHCYLIKPPDDNEFYNKQEALQHLIRSSGKLILLDKLLIRLR
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SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
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KTIQTISFLNYLFHEHQLYGPFLLRVPLSTLTSWQREIQTWAPQMNAVVYLGDITSRN
                    MIRTHEWMHPQTKRLKFNILLTTYEILLKDKSFLGGLNWAFIGVDEAHRLKNDDSLLY
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA linear PRI 07-DEC RP11-58M12, complete sequence.
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Pred. No. 1.9e-26;
0; Mismatches 0;
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Homo sapiens chromosome 5 clone
AC092372
AC092372.3 GI:17402768
HTG.
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/note="short i
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Unpublished
2 (bases 1 to 101220)
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Best Local Similarity 99.6%;
Matches 264; Conservative
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Direct Submission
L Submitted (10-10N-2001) Doos Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, (26 94598, usa)
E 4 (bases 1 to 114365)
E 5 Dob Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
L Submitted (12-10L-2001) Doos Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, (26 94598, usa)
Cocation/Qualifiers
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Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 134365)

DOB Joint Genome Institute and Stanford Human Genome Center.
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Bitren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barter, B., Linton, L., Nusbaum, C., Lander, P., Reda, F., Boquslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Changelo, M., Collins, S., Collymore, A., Cooke, P., Perreira, P., FitzHugh, W., Perrest, C., Gage, D., Galagan, J., Reristan, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Garaft, G., Hagos, B., Hadford, A., Horton, L., Hewland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
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1 (bases 1 to 143079)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, Clone RP11-58M12
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84.5%; Pred. No. 4.7e-18;
tive 0; Mismatches 40
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AC021449.3 GI:10047806
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                 Listing Completed at Stanford Human Genome Center

Ly Submitted (03-001-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 101220)

Established (03-001-2001) DOE Joint Genome Center.

Direct Submission

Ly Submitted (07-001-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94599, USA on Def 7, 2001 this sequence Version replaced gi:15290448.

Drive, Walnut Creek, CA 94599, USA on Def 7, 2001 this sequence Produced by DOE Joint Genome Institute

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Finishing Completed at Stanford Human Genome Center

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Homo sapiens chromosome 5 clone CTD-2082I17, complete sequence.
AC012624 6 GI:14993679
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2 (bases 1 to 134365)
Doe Joint Genome Institute.
Direct Submission
Submitted (31-0CT-1999) Production Sequencing Facility, DOE Joint
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DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
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Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McReheters, R., Maldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Submission

L. Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 10, 2000 this sequence version replaced gi:7407963.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center clone name: 58_M_12
Center clone name: 58_M_12
Sequencing vector: M13: M77815; 100% of reads
Sequencing vector: M13: M77815; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 134743 bases at least Q30
Consensus quality: 140814 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 144000; agarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
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106409: contig of 13793 bp in length
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75408: contig of 12689 bp in length
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/db_xref="fexxon:9906"
.clone="RP11-58M12"
/clone=lib="RPC1-11 Human Male BAC"
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กนบบชวง1
Homo sapiens chromosome 5 clone CTC-480Bll, WORKING DRAFT SEQUENCE,
7 ordered pieces.
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Unpublished
2 (bases 1 to 145659)
2 (bases 1 to 145659)
2 (bases 1 to 145659)
3 (bases 1 to 145659)
4 (bases 1 to 145659)
5 (bases 1 to 145659)
6 (103-40(-1999) Production Sequencing Facility, DOE Joint Submitted (103-40(-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA on Feb 14, 2001 this sequence version replaced gi:7528342.

Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
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Pred. No. 4.6e-18;
0; Mismatches 40;
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26246 c 26678 g 45278 t
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40512. .43279
/note="assembly_fragment"
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                                                                         47006. .51830
/note="assembly_fragment"
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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84.5%;
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Best Local Similarity
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Mon Aug

us-08-973-363-12.rge

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RESULT
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Summary Statistics

Consensus quality: 157767 bases at least Q40

Consensus quality: 180259 bases at least Q30

Estimated insert size: 204590, sqarcose-fp estimation

Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation

(Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 33 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
       AC091946 193446 bp DNA linear HTG 09-JUN-2001
Homo sapiens chromosome 5 clone RP11-36012, *** SEQUENCING IN
PROGRESS ***, 33 unordered pieces.
                                                                                                                                                                                                                                      our purished to 193446)

DOE Joint Genome Institute.

DOE Joint Genome Institute, Salo Mitchell Drive, Walnut Creek, CA 94598, USA Center: Joint Genome Center; Joint Genome Institute, Salo Mitchell Drive, Walnut Creek, CA 94598, USA Center: Joint Genome Institute
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                          Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
I (bases 1 to 193446)
DOB Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
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gap of unknown length

contig of 1209 bp in length

contig of 1056 bp in length

contig of 1056 bp in length

contig of 1957 bp in length

gap of unknown length

contig of 1977 bp in length

gap of unknown length

contig of 1672 bp in length

gap of unknown length

contig of 1064 bp in length

gap of unknown length

contig of 1064 bp in length

contig of 1064 bp in length

gap of unknown length

contig of 2100 bp in length

gap of unknown length

contig of 2051 bp in length

gap of unknown length

contig of 2051 bp in length

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contig of 1670 bp in length

gap of unknown length

contig of 1670 bp in length

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contig of 1870 bp in length

contig of 1870 bp in length
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Center clone name: RPCI-11_36012
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23515:
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HTG; HTGS_PHASE1.
human.
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Pred. No. 4.6e-18;
0; Mismatches 40; Indels 1;
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/clone="CTC-480B11"
/clone=lib="CalTech human BAC library C"
/26309 c 27580 g 48609 t 600 others
                              Project Information
Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
Web site: http://www.jgi.doe.gov
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Best Local Similarity 84.5%;
Matches 224; Conservative
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SHGC-58345 G38487
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                                                                                                         gap of unknown length
contig of 5514 bp in length
contig of 10422 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 5563 bp in length
gap of unknown length
contig of 7563 bp in length
contig of 7616 bp in length
gap of unknown length
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/clone_lib="RPCI human BAC library 11"
35252 c 37061 g 60360 t 3202 others
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contig of 7972 bp in length
gap of unknown length
contig of 6605 bp in length
gap of unknown length
contig of 6067 bp in length
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gap of unknown length
contig of 24237 bp in length.
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141644: gap of unknown length
169109: contig of 27465 bp in length
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gap of unknown length
contig of 5180 bp in length
gap of unknown length
contig of 9903 bp in length
                                                                                    unknown length
of 5982 bp in length
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130683: gap of unknown length
                                                          unknown length
of 4585 bp in length
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    193446
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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                     PRI 30-AUG-2001
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DOE Joint Genome Institute.

Direct Submission

Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 219258)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (30-A0G-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced g1:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walhult Creek, CA 94598, USA 4 (bases 1 to 219258) DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 219258)
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Homo sapiens chromosome 5 clone CTD-2007H13, complete sequence.
ACU22121
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Direct Submission
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Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
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84.5%; Pred. No. 4.1e-18;
Live 0; Mismatches 40
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42062 c 40933 g 64309
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/db_xref="taxon:9606"
/chromosome="5"
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/organism="Homo sapiens"
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Consensus quality: 260799 bases at least 030
Estimated insert size: 271581: sum-of-contigs estimation
Quality coverage: 8.62 in 020 bases; agarose-fp estimation
Quality coverage: 8.55 in 020 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 47 configs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                    ACU92382 276181 bp DNA linear HTG 03-JUL-2001
Homo sapiens chromosome 5 clone RP11-75H1, WORKING DRAFT SEQUENCE,
47 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

10 (bases 1 to 276181)

DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Uppublished
2 (bases 1 to 276181)

DOE Joint Genome Institute.
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1161: gap of unknown length
2827: contig of 1666 bp in length
2927: gap of unknown length
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Center clone name: RPCI-11_75H1
Db 87685 AGAAAAGACATAAAGGAAGAAAG 87661
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/organism="unknown"
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                Db 212172 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAATTAAAACAGAAAG-AGACAGTGA 212114
                                                                                                                                                                                                                211993 TATAAAGGAAAAGATTTTAAAGAAAAAAGAGAAAAAAAGAAAGTAAAAGGAAGCTATACAGAA 211934
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                                                                                                                                                  GATGAGATTGTTTCAGTGAAACATCTACATAAAAAATAAAAACAGAAAAAGAAAATGA
                                                                                                                                                                                                                                                                                                       181 ATTAAAAGAAAAGATAATAAAGAAAAGAGAGAAAACAAAGTAAAAGAATCCACACAGAA
                                                                                                    Length 276181;
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                                  /clone_lib="RPCI human BAC library 11"
51769 c 50026 g 82854 t 4673 others
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Pred. No. 3.9e-18;
0; Mismatches 40;
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Pred. No. 5.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 from Patent W09639505.
A58694
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10 c 33 g
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                         /clone="RP11-75H1"
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             /chromosome="5
                                                                                                 71.3%;
ilarity 84.5%;
Conservative
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Best Local Similarity 92.7%;
Matches 127; Conservative
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KEYWORDS
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                 PAT 28-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spastin, a novel AAA protein, is altered in the most frequent form of autosomal dominant spastic paraplegia
Nat. Genet. (1999) In press
2 (bases 1 to 179206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 179206)

Hazan,J., Fonknechten,N., Mavel,D., Paternotte,C., Samson,D.,
Artiguenave,F., Davoine,C.S., Cruaud,C., Durr,A., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Burgunder,J.M.,
Prud'Homme,J.F., Brice,A., Fontaine,B., Hellig,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGAGACAAA *120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ATTAAAAGAAAAAGATAATAAAGAAAAGAGAGAAAACAAAGTAAAAGAATCCACACAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 41.4%; Score 109.8; DB 6; Length 7218; Best Local Similarity 3.4%; Pred. No. 6.3e-07; Matches 9; Conservative 212; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                368 others
                 linear
                                                                                                                                                                                                                                 1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlbox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_DRAFT; SPG4 genomic DNA interval
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7218 bp 1
Sequence 14 from patent US 5670367.
166494
166494.1 GI:2724471
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14095 14194; gap of 100 bp 11195 14879 14978; contig of 684 bp in length 1479 14978; gap of 100 bp 100 bp 14979 14979 15664; contig of 686 bp in length
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17355: gap of
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15765 16456
16451 16550: 9
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1. Classes 1 to 72386)

1. Shiren.B.

2. (bases 1 to 72386)

1. Birren.B.

3. Harder.D., Nusbaum.C., Lander.E., Alli,A., Allen.N.,

4. Anderson.S., Barren.B.

4. Cameplano,A., Chang.J., Chazaro,B.,

Cochepel.Y., Colangelo.M., Collins,S., Collymore.A., Cook,A.,

Cooke,P., DeArellano,K., Dewar,K., Didaz.J.S., Dodge.S., Farc,S.,

Glade,S., Cord.B., Goyette,M., Graham.L., Grand-Pierre,N.,

Hagos,B., Heaford'A., Horton,L., Hulme.W., Illev.T., Johnson,R.,

Jones,C., Kamat,A., Karatas,A., Kells,G., Landcquer.R.,

Lamazares,R., Landers,T., Lehczky,J., Levine,R., Matthews,C.,

McCarthy, M., McGman,P., Marchis,C., Landcquer.B.,

McCarth,C., Mandonald,P., Major,J., Marquis,N., Matthews,C.,

McCarth,C., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Naylor,C.,

Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,

Raymond,C., Rotta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,

Raymond,C., Rotta,R., Santos,R., Santos, Schupback,R.,

Seaman,S., Severy,P., Spencer,B., Stanger-Thomann,N., Stojanovic,N.,

Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC102703 72386 bp DNA linear HTG 23-NOV-2001
MUS MUSCULUS CLONE RP24-442E5, LOW-PASS SEQUENCE SAMPLING
AC102703
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-442E5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 TATTGGTATAAAGAAGGAAGCTGAAGAAAAAAGAGAGAAAAGAGAAAAGAGAAATAAAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 GGAATTGAAAAGGGAGAAAAAAGAAAAAGGGGTAAGAAAGAATTAAAAGAAAAAGATAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AAACATCTACATAAAAAATAAAAACAGAAAAAAGAAAATGAAGAAAAGCCTGAGCCAGA 78
Submitted (29-FEB-2000) to the EMBL/GenBank/DDBJ databases on Mar 6, 2000 this sequence version replaced gi:6981752. Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                               Query Match 40.9%; Score 108.4; DB 9; Length 179206; Best Local Similarity 65.0%; Pred. No. 4.2e-07; Matches 160; Conservative 0; Mismatches 86; Indels 0;
                                                                                                                                                                                                                                           2000 others
                                                                                                                                                        /chromosome="2"
/clone=11b="CITB_978_SKB"
/clone=1367K01"
a 36514 c 37908 g 52090 t
                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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HTG; HTGS_PHASE0.
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AC102703/c
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Center: Whitehead Institute/ MIT Center for Genome Research Center: Whitehead Institute/ MIT Center for Genome Research Web site: https://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Center project Information Center project name: L19314 Center clone name: 442_E_5
Topham, K., Travers, M., Travis, N., Trigillo, J., Vassillev, H., Viel, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Direct Submission
Direct Submission
Direct Submission
Direct Submission
Research 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Sh. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This record contains 92 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-ritch and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* this beginned to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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of 681 bp in length
100 bp
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of 689 bp in length
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of 100 bp contig of 686 bp

con. ; gap of 7255: 6450: cont

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18053 18150 3 contigo of 713 bp in length 18664 19963; gap of 713 bp in length 18664 19963; gap of 713 bp in length 18665 19775 20457; contig of 683 bp in length 19775 19745; contig of 683 bp in length 20588 20573; gap of 100 bp in length 20588 20573; gap of 100 bp in length 20588 20573; contig of 679 bp in length 22855; gap of 100 bp in length 22858 20573; contig of 679 bp in length 22858 20573; contig of 679 bp in length 22858 20573; contig of 679 bp in length 22858 20573; gap of 100 bp in length 22858 20573; gap of 100 bp in length 22859 20593; contig of 679 bp in length 2373 2736; gap of 100 bp in length 2520 20519; gap of 100 bp in length 2520 20599; gap of 100 bp 
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44845: contig of 672 bp in length
44845: gap of 100 bp
45633: contig of 688 bp in length
45733: gap of 100 bp
46449: contig of 716 bp in length
contig of 695 bp
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PAT 05-OCT-2001
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Epigenomics AG (DE)

Location/Qualifiers

1 . 24259

/organism="synthetic construct"
/db_xref="taxon:35630"
/note="chemically treated genomic DNA (Homo sapiens)"
/75 c 5732 g 11760 t
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 72386;
46450 46549: gap of 100 bp 47245: contig of 696 bp in length 47246 47345: gap of 100 bp 47346 47345: gap of 100 bp 48021: contig of 676 bp in length 48022 48121: gap of 100 bp 48122 48944: gap of 100 bp 49575 48945: gap of 100 bp 49575 4974: gap of 100 bp 50372 50471: gap of 100 bp 51263 51263: gap of 100 bp 51263 51263: gap of 100 bp 51263 52721: contig of 684 bp in length 51263: gap of 100 bp 52722 52821: gap of 100 bp 52822 52821: gap of 100 bp 52832 53595: gap of 100 bp 53896 53695: gap of 100 bp 53896 53695: gap of 100 bp 53896 53896: contig of 674 bp in length 53896 53800: contig of 674 bp in length 53896 53800: contig of 679 bp in length 53896 53800: contig of 679 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 103.2; DB 2;
Pred. No. 2.7e-06;
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synthetic construct
artificial sequence.
[ lases 1 to 24259]
Olek,A., Piepenbrock,C. and Berlin,K.
Diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oncogenes
Patent: WO 0168912-A 415 20-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Sequence 415 from Patent W00168912.
AX251447
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                                                                                                                                                                                                                                                                                                                                                                                                                         38.9%;
62.2%;
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* NOTE: This record contains 75 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced
* However, it should not be assumed that this clone
* thill be sequenced to completion. In the event that
* the record is updated, the accession number will
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Shiren, B. Lintcon.L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Capuslavkiy, L., Boukhater, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Gobepel, Y., Collins, S., Collymore, A., Cocke, P., Dehrellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Deyle, M., Cocke, P., Calagan, J., Garaham, E., Grand-Elerre, N., Grand, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Klein, J., Lilly, I., Johnson, R., Jones, C., Kan, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Leboczky, J., Levine, R., Leu, C., Lilly, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGart, A., McKernan, K., McDeczky, J., Levine, R., McEwan, F., McGurt, A., McManan, R., McDecky, J., Levine, R., McEwan, P., McGurt, P., Wolrow, J., Naylor, Norman, C., Holl, O., Obonnell, P., Obliara, V., Santos, R., Seper, P., Spencer, B., Stange-Thoman, N., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thoman, N., Santos, J., Tirrell, A., Travers, M., Trigillo, J., Veshilev, H., Viel, R., Vol, N., Viel, R., Vol, N., Winson, B., Wu, X., Wyman, D., Ye, W., Viel, R., Viel, R., Vol, N., Viel, R., and Sody, M., Stannon, J., Zimmer, A. and Sody, M., Sunon, J., Zimmer, A. and Sody, M., Stannon, J., Zimmer, A. and Sody, M., Stannon, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACU23852 60565 bp DNA linear HTG 09-DEC-2000 SEQUENCE SAMPLING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 60565)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo saplens chromosome 8, clone RPII-106572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (18-FBE-2000) Whitehead Institute/MIT Center for Genome Submitted (18-FBE-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 9, 2000 this sequence version replaced gi:9157739.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                               ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 GGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGAAAAAAGAAAAAGAAAATAAAAGGGAA 142
                                                                                                                                                                                                                                                                                                                                                        Local Similarity 64.0%; Pred. No. 4.1e-06;
nes 155; Conservative 0; Mismatches 87;
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Web site: http://www-seq.wi.mit.edu
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AC023852.3 GI:11610937
HTG; HTGS_PHASE0.
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AC023852/C
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DEFINITION
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
REFERENCE
AUTHORS
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Preserved. 719: contig of 719 bp in length 720 819; gap of 100 bp 820 1525: contig of 720 bp in length 1526 1625; gap of 100 bp 100 bp 3131 3205; gap of 100 bp 313 3205; gap of 100 bp 3205; gap of

in length in length

50: gap of 100 bp 22560: contig of 710 bp 60: gap of 100 bp 23368: contig of 708 bp

22660:

139 GGAATTGAAAAGGGAGAAAAAAGAAAAAGGGATAAGAAAGAATTAAAAAGAAAAAGATAA 198 79 TATTGGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGAGACAAAAGAGAAAATAAAAG 138 19 AAACATCTACATAAAAAAATAAAAACAGAAAAAGAAAATGAAGAAAAGCCTGAGCCAGA 78 ö Length 60565; Indels 52652 53343: contig of 692 bp in length 53344 53443: gap of 100 bp 54171: contig of 728 bp in length 54172 54271: gap of 100 bp 54272 55931: gap of 100 bp 55032 55031: gap of 503 bp in length 55032 55736: contig of 705 bp in length 38.7%; Score 102.6; DB 2; ilarity 61.0%; Pred. No. 3.4e-06; Conservative 0; Mismatches 96; Best Local Similarity Matches 150; Conser 31174 AAAAAA 31169 259 AGAGAA 264 Query Match g ŏ ŏ QQ ò qq g

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Search completed: August 2, 2002, 20:58:08 Job time: 26729 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Chicken CHD-1A ins	Chicken CHD-W clon	Tumour suppressor	Human immune syste	Human immune syste	Base sequence of t	Base sequence of t	Cowpox virus bsr f	Base sequence of t
SUMMARIES	AAT42752	AAT42753	AAS46691	ABL33697	ABL34174	AAX33181	AAX33182	AAX33180	AAX33184
DB	18	18	22	24	24	20	20	20	50
% Query Match Length DB	265	137	24259	6668	113515	6644	7372	7797	1996
% Query Match	100.0	46.3	38.8	38.5	38.5	38.3	38.3	38.3	38.3
Score	265	122.6	102.8	102	102	101.4	101.4	101.4	101.4
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ABL3278 ABL33704 ABL33404 ABL33958 ABL33958 AAS65367 AAS65367 ABL33808 ABL33808 ABL33808 ABL33808 ABC33808 ABC33808 ABC33808 ABC33808 ABC352236 ABC352236 ABC352236	AANG 9384 ABL 33126 ABL 33126 ABL 34175 ABL 34175 ABL 3408 ABL 33189 ABL 3888 ABL 3888	LIGNW bind bind disru
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                                                                                                                                                                                                                                                                                                                                            61 AGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGAGACAAAA 120
                                                                                                                                                                                                                                                                                  A composite nucleotide sequence (AAT42752) and putative translation (AAW08144) sequence are provided of a motif that is found spliced to a proportion of chicken CHD-1A clones. The motif is inserted between bases 4327 and 4328 of the CHD-1A composite sequence (AAT42751). None of the 7 CHD-1 clones examined contained the complete motif. There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary CHD-W clone CC14 (see also AAT42753).
                                                                                                                                                                                                                                                sex determination; chromodomain-Helicase-DNA binding 1 Avian;
  chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                       /*tag= a
/note= "base 52 disrupts the reading frame for
the translated amino acid sequence given
                                                                                                                                                                                                                      ó
                                         Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                    Length 265;
                                                                                                                                                                                                                      Indels
                                                                                                                                                                          Sequence 265 BP; 158 A; 16 C; 61 G; 30 T; 0 other;
                                                                                                                                                                                                   100.0%; Score 265; DB 18;
100.0%; Pred. No. 1.4e-31;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                241 agaaaaagaagtgaaggaagaag 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken CHD-W clone CC14 3' motif.
                                                                    Disclosure; Fig 7; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                               241 AGAAAAAGAAGTGAAGGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT42753 standard; cDNA; 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                      265; Conservative
Griffiths R, Tiwari
                                                                                                                                                                                                             Similarity
                WPI; 1997-043127/04
                         P-PSDB; AAW08144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus sp.
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                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHD-W;
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A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAM08145) sequence are provided of a motif that is found spliced to the 3' end of chicken CHD-W clone CC14 (see also AAT42754). There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found as an insert in some CHD-IA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGAGACAAA 120
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0
                                                                                                                                                                                                                                                                 Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.3%; Score 122.6; DB 18; Length 137; 93.4%; Pred. No. 2.2e-10; Live 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .. 2e-10;
9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 137 BP; 75 A; 10 C; 34 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 7; 76pp; English.
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
96WO-GB01341.
                                             95GB-0011439.
                                                                                             (ISIS-) ISIS INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                          Griffiths R, Tiwari B;
                                                                                                                                                                                          WPI; 1997-043127/04.
P-PSDB; AAW08145.
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nes 128; Conserv
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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05-JUN-1996;
                                             06-JUN-1995;
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                                                                                                                                                                                                                The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since nuclears having a sequence taken from 536 (actually 533 since mapers 408, 458 and 500 are missing from the sequence listing) sequences (CS) and sequences complementary to (SS). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleides and may compared to a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in a method for cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters which are disadvantageous to patients. The present sequence is one of the consequences sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID), ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó;
                                                                                                 Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 GGTATAAAGAAGGAAGCTGAAGAAAAAAGAGACAAAAGAGAAAGGAAAATAAAAGGGAA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 ATCTACATAAAAAATAAAAACAGAAAAAAGAAAATGAAGAAAAAGCCTGAGCCAGATATT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24259 BP; 6392 A; 375 C; 5732 G; 11760 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
1e-07;
87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                       Claim 1; SEQ ID No 414; 27pp; English.
                                   Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL33697/c
ID ABL33697 standard; DNA; 6668 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 64.0 les 155; Conservative
                              Piepenbrock C,
                                                                WPI; 2001-602752/68.
(EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11895 AA 11894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID 2 and ID
is missing)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                 olek A,
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer, si disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
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                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic; antiatretriosotatic; nootropic; antiatretriosotatic; nootropic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologic; anti-HIV; antiatric; antidiabetic; antipsoriatic; antififammatory; cancer; eye disease; arteriosotalerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1670; 32pp + Sequence Listing; German.
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                                                            Human immune system associated gene SEQ ID NO: 1670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2001; 2001WO-EP07537.
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01-SEP-2000; 2000DE-1043826.
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic; antiatensemic; oytostatic; nootropic; neutanaemic; oytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; optthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinfammatory; cancer; eye disease; arteriosclarosis; anaemia; acute myeloid leukaemia; Alzheiner's disease; Arteriosclarosis; anaemia; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 113515 BP; 31803 A; 1174 C; 24020 G; 56518 T; 0 other;
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                                                                                                                                                                                                                              Human immune system associated gene SEQ ID NO: 2147.
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Pred. No. 1.1e-07;
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                   26-MAR-2002
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                                                                                                          ABL34174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
                          ABL34174/c
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis associated genes. These can then be used in a variety of diseases for which the induction of apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressing an apoptosis associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \rho Rx\text{-}ires\text{-}bsr, which contains the cowpox virus bsr gene, and in an example from the present invention.
                                                                                                                                                                                                                                                                                     Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20; Length 6644;
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96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New apoptosis-resistant virus-sensitive cell
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Best Local Similarity 62.4%; Pred. No. 1.9e-
Matches 159; Conservative 0; Mismatches
                                                                                                                                                                                                                                                Base sequence of the plasmid pRx-ires-bsr.
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                                                                                                                                    BP.
                                                                                                                                   DNA; 6644
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                                                                                                                                                                                                                                                                                                                                             inflammatory disease; ss
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                                                                                                                                   AAX33181 standard;
                                     51483 AAAAAA 51478
259 AGAGAA 264
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                                                                                                                                                                                                                                                                                                                                                                                                         Cowpox virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-SEP-1997;
                                                                                                                                                                                                            25-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                        AAX33181;
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Hamada H;
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call line into which an apoptosis resistance gane has been introduced.
The recombinant viruses generated are capable of expressing apoptosis-
associated genes. These can then be used in a variety of diseases for
which the induction of apoptosis by gene transfer, or where the
inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
the useful as vectors for gene therapy which can be applied to cancer
therapy for destroying cancer cells selectively, the treatment of
autoimmume diseases and graft rejection reaction, and apoptosis induction
therapy for inflammatory cells in inflammatory diseases. Prior arts have
concountered the problem where if an adenovirus vector capable of
concountered the problem where if an adenovirus vector capable of
the required to induce cell death by apoptosis is shorter than that
the required to replicate and produce the virus will be destroyed because the period of
time required to replicate and produce the virus will be destroyed apoptosis-associated
cobtain a recombinant virus having the integrated apoptosis-associated
gene. In this invention an apoptosis-resistant 293 cell line (having an
                                                                                                                                                          3853
                                                                                                                                                                                                                                                                ||| |||| |||| ||| || ||| || ||| || ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || 
189
                                                                                                                                                                                                                                                                                                                                                       249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmh, bcl.2, bcl.2, bcl.2, bcl.2, bcl.3, autoimmune disease; graft rejection reaction; inflammation; inflammatory disease; ss.
                                                                                          130 AAATAAAAGGGAATTGAAAAGGGAGAAAAAAGAAAAAGGGATAAGAAAGAATTAAAAGA
                                                                                                                                                                                                                                                                                                                                                   Base sequence of the plasmid pRx-Bcl-xl-bsr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New apoptosis-resistant virus-sensitive cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 41-45; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RPRG-) RPR GENCELL ASIA PACIFIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX33182 standard; DNA; 7372 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-JP04010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3974 aaaaaaaaaaaaa 3988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTGAAGGAAGAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-243728/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamada H;
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The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 AAATAAAAGGGAATTGAAAAGGGAGAGAAAAAGAAAAAGAGGGATAAGAAAGAATTAAAAGA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                               10 GTTTCAGTGAAACATCTACATAAAAAATAAAAACAGAAAAAAGAAAATGAAGAAAAGCC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmh, bcl-2; bcl-Xi; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation; inflammatory disease; ss.
apoptosis resistant gene introduced) is established and overcomes problem. The present sequence represents the base sequence of the plasmid pRx-Bcl-xl-bsr, which contains the human Bcl-xl gene, and is used in an example from the present invention.
                                                                                                                                                                                                                            38.3%; Score 101.4; DB 20; Length 7372; Similarity 62.4%; Pred. No. 1.9e-07; S9; Conservative 0; Mismatches 96; Indels 0;
                                                                                                                                          Sequence 7372 BP; 2353 A; 1749 C; 1649 G; 1621 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New apoptosis-resistant virus-sensitive cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cowpox virus bsr full length gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 34-38; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RPRG-) RPR GENCELL ASIA PACIFIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX33180 standard; DNA; 7797 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-JP04010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-243728/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cowpox virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09913073-A2.
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                                                                                                                                                                                                                                                                 Best Local Sim:
Matches 159;
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inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction the contract of the
                                                                                                                       therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of encountered the problem where if an adenovirus vector capable of the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the cowpox virus ber gene which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAGCCAGATATTGGTATAAAGGAAGGTAGCTGAAGAAAAAAAGAGACAAAAGAGAAGGA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAAGATAATAAAGAAAAAGAGAAAACAAAGTAAAAGAATCCACACAGAAAAGAAAAAGA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 GITICAGIGAAACAICIACAIAAAAAATAAAAACAGAAAAAAGAAAAIGAAGAAAAGCC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7797;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7797 BP; 2542 A; 1760 C; 1656 G; 1839 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.3%; Score 101.4; DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Base sequence of the plasmid pRx-Bcl 2-i-hCD 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RPRG-) RPR GENCELL ASIA PACIFIC INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5127 aaaaaaaaaaaaa 5141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTGAAGGAAGAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9913073-A2
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Hamada H;

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The recombinant viruses generated are capable of expressing apoptosis resistance gene has been introduced.

The recombinant viruses generated are capable of expressing apoptosis associated genes. These can then be used in a variety of diseases for which the induction of apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of expressing an apoptosis associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that could contain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence of the plasmid pRx-Bol 2:1-hCD 25, which contains the human Bcl-2 gene, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 TGAGCCAGATATTGGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGAGAAAAAAGAGAAAGGA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 GTTTCAGTGAAACATCTACATAAAAAATAAAAACAGAAAAAAGAAAATGAAGAAAAAGCC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhemmatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7996 BP; 2463 A; 2015 C; 1829 G; 1689 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.3%; Score 101.4; DB 2U; 62.4%; Pred; No. 1.9e-07; wiematches 96;
                                                           New apoptosis-resistant virus-sensitive cell
                                                                                                   Example 3; Page 46-49; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL32788 standard; DNA; 6171 BP
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Best Local Similarity 62.49
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5326 aaaaaaaaaaaaaa 5340
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ABL32788/c
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelold leukaemia, Alzheimer, disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 TATTGGTATAAAGAAGGAAGCTGAAGAAAAAAGAGAGACAAAAAGAGAAAAATAAAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 GGAATTGAAAAGGGAGAAAAAAAAAAAAAAGAGATAAAGAAATTAAAAGAAAAAGATAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
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                   antiarterioscleritic; antianaemic; cytostatic; nootropic; neuroprofective; anti-HTV; anticonvalsant; ophthalmological; antitheammatic; antiarthritic; antidiabetic; antipsoriatic; antinifammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; Albs; epilepsy; heurofibronatosis; heurofilorodi arthritis; psoriasis; bowel disease;
Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
37.9%; Score 100.4; DB 24; Length 16033;
Best Local Similarity 63.0%; Pred. 70. 2.4e-07;
Matches 155; Conservative 0; Mismatches 91; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16033 BP; 3610 A; 352 C; 4561 G; 7510 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1377; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
ABL33719/c
ID ABL33719 standard; DNA; 17934 BP.
XX
                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000; 2000DE-1032529.
                                                                                                                                                                                                                                                                                                                                                        02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 AGAGAA 264
                                                                                                                                                                                                                                                             WO200200928-A2.
                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch al Similarity 62.1%; Score 100.8; DB 24; Length 6171; al Similarity 62.1%; Pred. No. 2.4e-07; 1169; Conservative 0; Mismatches 97; Indels 0; 159; Conservative 0; Mismatches 97; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6171 BP; 1614 A; 118 C; 1339 G; 3100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 761; 32pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                 Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL33404 standard; DNA; 16033 BP.
                                                                                                                                                                                                            02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                           30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AAGTGAAGGAAGAGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 AAAAAAAAAAAA 361
                                                                                                                                                                                                                                                                                                                                                                            Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytosine methylation
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                                                                                                                   WO200200928-A2.
                                                                          Homo sapiens.
                                                                                                                                                                  03-JAN-2002.
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                           gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17934 BP; 4426 A; 283 C; 4402 G; 8823 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 1692; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91; Indels
                               Human immune system associated gene SEQ ID NO: 1692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .4e-07;
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Pred. No. 2.4e-
0; Mismatches
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01-SEP-2000; 2000DE-1043826.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytosine methylation
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155; Conserv
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                                                                                                                                                                                                                                      WO200200928-A2.
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                                                                                                                                                                                                            Homo sapiens.
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                  immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1931; 32pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 1931.
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62.8%; Pred. No. 3e-07;
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Pred. No. 3e-07;
___thes 92;
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                                                                BP.
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                                                             ABL33958 standard; DNA; 14006
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Matches 155;
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80 ATTGGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGAGACAAAAGAGAAGAAAATAAAAGG 139

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO19310) that exhibit extivity elating to grother proliferation or call differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodiatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp, wipo.int/pub/published_pct_sequences.
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 2739; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 2739.
                                                                                                                                                                         AAI82679 standard; cDNA; 329 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fang YT, Liu C, Drmanac RT;
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18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                  06-NOV-2001 (first entry)
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                                                                                   2061 AAAAAA 2055
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                                                  258 AAGAGAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200164835-A2.
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AAI82679/c
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20 AACATCTACATAAAAAAATAAAAACAGAAAAAAAAAATGAAAAAAGCCTGAGCCAGAT 79

37.6%; Score 99.6; DB 22; Length 329; 61.2%; Pred. No. 5.1e-07; tive 0; Mismatches 95; Indels 0; Gaps

Best Local Similarity 61.2% Matches 150; Conservative

Query Match

Sequence 329 BP; 21 A; 14 C; 12 G; 271 T; 11 other;

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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases of a segment of the chemically pretreated but A of genes associated with metabolism such as DUSP2 (NM_00418). EPRX2 (NM_00199), COPR (NM_000320), SGSH (NM_000199), SHWT2 (NM_0005412), SLC7A2 (NM_000464), SLC7A4 (NM_000199), SHWT2 (NM_001917) (all copper 
Human, cytostatic; anti-tumour; metabolism; metabolic disease; liver; solid tumour; cancer; cytosine methylation; epigenetic; eye; Kidney; single nucleotide polymorphism detection; SNP; stool; urine; lung; cerebral-spinal fluid; intestine; brain; heart; prostate; breast; DUSP2; EPHX2; ODPR; SGSH; SHMT2; SLC7A2; SLC7A4; TYMS; ds.
                                                                                                                                                                                                      New nucleic acid, useful for diagnosis and therapy of metabolic disease, solid tumour and cancers, comprises segment of chemically modified genomic sequences of genes associated with metabolism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemically pretreated metabolism associated gene #62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 141-142; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olek A, Piepenbrock C, Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS63367 standard; DNA; 3586 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-2001; 2001WO-EP04016.
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                                                                                                                                                                                                                                                                                       260 GAGAA 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
AAS63367/c
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unmethylated at the 5th-position are converted to uracil or another base which is dissimilar to cytosine in terms of hybridisation behaviour and amplifying fragments of the chemically pretreated genomic DNA. The genomic DNA is from cells or cellular components which contain DNA, sources of DNA comprising, for e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eye, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides and their combinations. Genetic parameters are mutations, in particular insertions, deletions, point metabolism and sequences further required for their regulation.

Epigenetic parameters are in particular cytosine methylations and further chemical modifications of DNA bases of genes associated with metabolism. Further epigenetic parameters include for their regulation.

Epigenetic parameters are in particular cytosine methylations and further epigenetic parameters include for e.g. the acetylation of histones which correlates with DNA methylation.

AAS63306-AAS63373 represent chemically pretreated metabolism associated constants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 TATTGGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGAGACAAAAGAGAAAATAAAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 GGAATTGAAAGGGAGAAAAAAGAAAAAAGGATAAGAAAGAATTAAAAGAAAAGATAA 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 AAACATCTACATAAAAAATAAAAACAGAAAAAAGAAAATGAAGAAAAGCCTGAGCCAGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.4%; Score 99.2; DB 24; Length 3586; 64.2%; Pred. No. 4.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3586 BP; 1063 A; 22 C; 636 G; 1865 T; 0 other;
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Matches 149; Conserv
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Search completed: August 2, 2002, 20:53:00 Job time: 26271 sec

104.8 39.5 614 12 AG327327 AG37327 Dbxb0040D AG04222 Pan trog1 AG04222 Pan trog1 AG04222 Pan trog1 AG04366 AG063366 AG263366 AG263366 AG263366 AG263366 AG263366 AG263366 AG263366 AG263366 AG263366 AG263242 AG67342 AG67342 AG67342 AG67342 BG734242 BG73442 BG73442 BG73442 BG73442 BG73442 BG73442 BG73442 BG73442 BG734442 BG7344442 BG734442 BG7344442 BG7344442 BG73444442 BG73444442 BG73444444 BG734444444 BG73444444 BG73444444 BG7344444444 BG734444444 BG73444444 BG73444444 BG7344444444 BG734444444	39.2 952 12 CNSO14BF 39.2 431 12 CNSO17W2 39.2 830 3 BIG45072 39.2 966 10 BM415686 39.1 723 12 CNSO06OI 39.1 868 12 AZ54418 39.1 979 12 AZ538989	1 BM015597
0 00 0 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0	388 399 444 444 844 844 844 844	RESULT 1 BM015597 LOCUS DEFINITION ACCESSION VERSTON KETWORDS SOURCE ORGANISM REFERENCE ACTIVE JOHNNAL COMMENT COMMENT SOURCE SOURCE SOURCE
sion 4.5 000 Compugen Ltd. del 13 ; Search time 894 (without align 400.050 Millio	r chosen parameters: 27472414 100 1008 45 summaries	results predicted by chance to have a 1 to the score of the result being printed, of the total score distribution. SUMMARIES ID Description ID Description ID Description ID Description A7242163 A7242163 A744863 A744863 A744863 A744863 A744863 A74429 BH01559 BH016129 BH016129 BH016129 BH016129 AG04722 BH01612 OPD21229 HA69918 AG04725 AG04725 AG04725 AG04865 AG04865 AG04865 AG04865 AG04865 AG04865 AG04865 AG04865 AG04865 AG04866 AG04869 AG04866 AG04869 AG04868 AG04869 A
Gersearch, usisearch, usist 2, 2002 Search, usist 2, 2007 Search,	ngth: 0 mgth: 0 mgth: 20000000 mgth: 20000000 Minimum Match (Maximum Match) Listing first (EST:*	mm_estba:* em_esthum::* em_esthum::* em_esthum::* em_estpl:** em_estpl:** em_estpl:** gb_estl:** gb_estl:** gb_htc:** gb_htc:*
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Gaps

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Length 821;

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q30 bp mRNA linear EST 01-DEC-1998 qh81f02.x1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:1851099 3' similar to contains element LTR5 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1274 Std Error: 0.00
Seq primer: 400P from Gibco
High quality sequence stop: 429.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   121 AGACAAGGAAAATAAAAGGGAATTGAAAAGG-CAGAAAAAAGAAAAAAGAGGATAAGAAAG 179
                                                                                                                                                                                                                                                                                                          354 AGAAAAGGAGAATAAAAAAGAACTTAAAAGGTGAGATAAAAGAAAAAAAGAGGATAAGAAAG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)." 149~c~190~q~137~t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATTAAAAGAAAAAGATAATAAAGAAAAGAGAGAAAACAAAGTAAAAGAATCCACAGA
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/db_xref="texton:9606"

/clone="IMAGE:1851099"

/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
                                                                                                                                                                                                                           54; Indels
                                                                                                                                                                        DB 10;
                                                                                                                                                                   Score 151.6; DB 1
Pred. No. 3.8e-07;
0; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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78.0%;
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KEYWORDS
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/clone="Inage:413129"
/clone="Inage:413129"
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/clone="Inage:4129
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E I (bases 1 to 821)
S NIH-MCC http://mgc.noi.nih.gov/.
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Capabs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC column: 18
High quality sequence stop: 562.
Location/Qualifiers
Irce //organism="Homo sapiens"
//db.zeref="Hexon:866"
//db.zeref="Hexon:866"
//db.zeref="Hexon:866"
//db.zeref="Hexon:866"
//db.zeref="Hexon:866"
//db.zeref="Hexon:866"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGAGACAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                   1 GATGAGATTGTTTCAGTGAAACATCTACATAAAAAATAAAAAACAGAAAAAAGAAAATGA 60
                                                                                                          Length 677;
                                                                                                                                                                40; Indels
                                                                                                             DB 10;
                                                                                                                                       Pred. No. 1e-09;
                                                                                                                                                                0; Mismatches
  127
                                                                                                             Score 178;
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  153
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                                                                                                          67.2%;
84.2%;
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                                                                                                                                                             Matches 224; Conservative
  92
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305
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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Mon Aug

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us-08-973-363-12.rst

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Bonaldo, Ph.D.

CORM Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.E. Consortium/LINL at:
www.bio.llnl.gov/Drp/image/image.html
Insert Length: 1312 Std Error: 0.00
Seq primer: -40013 fwd. Er from Amersham
High quality sequence stop: 282.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anote-"Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RT: 1st strand cDNA was prepared from luman tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA48563
343 bp mRNA linear EST 27-JAN-1998 oa5/CO9.s1 NCI_CGAP_GCB1 Homo saplens CDNA clone IMAGE:1309072 3' similar to SW:CHD1_MOUSE P40201 CHROMODOMAIN-HELICASE-DNA BINDING PROTEIN CHD-1. [1] ;contains element L1 repetitive element ;, mRNA
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Eukaryota; Menazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mamanalia; Eutera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 343)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
     Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement. Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                              1 GATGAGATTGTTTCAGTGAAACATCTACATAAAAAAATAAAAAACAGAAAAAAGAAAATGA 60
                                                                                                                                                                                                                                                                                                                                                                                                              and Eco RI sites of the modified pT7T3 vector. Lib
Went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                         11arity 84.18; Pred. No. 3.18-06; Length 430; Conservative 0; Mismatches 32; Indels 1
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/Abxref="texon:9606"
/clone="IMAGE:1309072"
/clone=lip="NOI_CGAP_GCB1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ATTAAAAGAAAAGATAATAAAGAAAA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 TATAAAGGAAAAGATTTTAAAGAAA 1
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AA748563.1 GI:2788521
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Unpublished (1997)
                                                                                                                                                                                                 Best Local Similarity
Matches 174; Conserv
                                                                                                                                                                            Query Match
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456 bp mRNA linear EST 19-DEC-1997 zi6f112.sl Soares_fetal_liver.spleen_lNFLS_Sl Homo sapiens CDNA clone lHAGE:435311 3', mRNA sequence.
AA69918.1 GI:2702881
1;
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1 (bases 1 to 456)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,T., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: estéwatson wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                   Ouery Match 53.7%; Score 142.2; DB 9; Length 343; Best Local Similarity 83.6%; Pred No. 5.1e-06; Matches 173; Conservative Namatches 33; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:1335080"
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Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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40.7%; Score 107.8; DB ilarity 64.8%; Pred. No. 0.0083; Conservative 0; Mismatches 8
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           'db_xref-"taxon:36090"
                                                                                              potato cyst nematode"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: warthog@unity.ncsu.edu
GT11PCN1_G06_1-42F_040.abl.
Location/Qualifiers
                                                                                                                                                  Query Match
Best Local Similarity
Matches 160; Conserv
                                                                                                                                                                                                                                                                                                                                                                     258 AAGAGAA 264
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      1;
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
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                                                                                                                                                                                                                                                                                        Heer J., Sosinski B., Pokrzywa R.M., Warry A., Opperman C., "Mixed Stage EST's from Globodera pallida, the potato cyst nematode";
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                       1 GATGAGATTGTTTCAGTGAAACATCTACATAAAAAATAAAAACAGAAAAAAGAAAATGA 60
                                                                                                                                                                                                                                                                      84
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Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
                                                                                                                                                              Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: warthog@unity.ncsu.edu
No homology found. ; GT11PCN1_G06_1-42F_040.abl.seq.screen.
                                                                                                                                                        ; DB 9; J
.6e-06;
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13-SEP-2001 (Rel. 69, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Opperman, C
Center for the Biology of Nematode Parasitism
NC State University; IACR-Rothamsted
Campus Box 7616; Raleigh, NC 27695, USA
Fax: 919.515.9500
                                                                                                                                                            Score 139.8; I
Pred. No. 7.6e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              standard; RNA; EST; 851 BP.
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                                                                                                                                                             52.8%;
                                                                                                                                                            Query Match 52.8 Best Local Similarity 83.7 Matches 170; Conservative
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OP21229 Mixed Stage EST's from Globodera pallida, the potato cyst nematode Globodera pallida, the potato cyst BM416142
BM416142
EST. 8 From Globodera pallida cDNA, mRNA sequence.
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Clone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode"

/note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsred and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs,
/note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage Gpallida in lambda GT11 by Paul Burroughs,
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Globodera pallida
Eukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Heteroderidae, Heteroderinae, Globodera.
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                                                                                                  FACR-Rothamsted."
/organism="Globodera pallida"
/clone_lib="Mixed Stage EST's from Globodera pallida,
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Hear J., Sosinski,B., Pokrzywa,R.M., Warry,A.
Mixed Stage EST's from Globodera pallida, the
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Opperman, C
Center for the Biology of Nematode Parasitism
NC State University; IACR-Rothamsted
Campus Box 7616; Raleigh, NC 27695, USA
Tel: 919.515.9500
                                                                                                                                                                                                                                       Sequence 851 BP; 114 A; 72 C; 15 G; 615 T; 35 other;
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Pulyman A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Matanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AdG-2001) Asao Fuliyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-Chou, Tsurumiku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbesegsc.riken.go.jp, NR.Litte://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Glones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AG047727 697 bp DNA linear GSS 02-NOV-2001
Pan troglodytes DNA, clone: PTB-027F10.F, genomic survey sequence.
AG047727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AG047727.1 GI:16584619
GSS: GSS (qenome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-027F10.F.
Pan troglodytes
BLAATYOCES.
Manmalla: Eutheria: Primates; Catarrhini; Hominidae; Pan.
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11/jama.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end Sequences of Library PTB
                                                                         Score 107.8; DB 10; Length 982;
Pred. No. 0.0077;
0; Mismatches 87; Indels 0;
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/ba_xref="taxon:9598"
/clone="PTB-027F10.F"
/sex="male"
/coll_type="lymphoblast"
/clone_llb="PTB Chimpanzee Male BAC Library"
                39 others
              646 t
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IACR-Rothamsted."
198 a 78 c 21 g
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                           Query Match
Best Local Similarity 64.8%;
Matches 160; Conservative
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2. (bases 1 to 812)

Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail:chimpbesggsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/;

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
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                                                                              40.3%; Score 106.8; DB 12; Length 697; 64.6%; Pred. No. 0.012;
tive 0; Mismatches 87; Indels 0;
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/ 53 c 61 others
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/db_xref="taxon:9598"
/clone="PTB-022M24.R"
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14 CAGTGAAACATCTACATAAAAAATAAAAACAGAAAAAAGAAAATGAAGAAAAAGCCTGAG 73
                               Score 106.4; DB 12;
Pred. No. 0.012;
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Best Local Similarity 60.33
Matches 149; Conservative
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                               Query Match
Best Local Similarity
Matches 158; Conserv
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-045720.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (N2-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-603-9170)
Telones are derived from the chimpanzee BAC library PTB This BAC end was generated during the RsD process and may have higher chance of
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                   Gaps
                                                                                                        Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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                                            Length 812;
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                                             DB 12;
                                            Score 106.4; DB Pred. No. 0.012;
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Pujiyama,A., Hattori,M., Toyoda,A., T
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished

    .820
    /organism="Pan troglodytes"
/db_xref="taxon:9598"
    /clone="PTB-045J20.F"

                                                                          0; Mismatches
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanze
29 c 86 g 21
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence T7 end of BAC BACN16402 of DrosBAC library from Drosophila melanogaster (fruit Ily), genomic survey sequence.

AL107011
AL107011, GI:5624989
                                                                                                                                                                             134 AAAAGGGAATTGAAAAGGGAGAAAAAAGAAAAAGAGGATAAGAAAGAATTAAAAGAAAA 193
Gaps
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                                                                                                                                                                                                                                                                                                 74 CCAGATATTGGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGACAAAAGAGAAAAT
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN16H02"
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79 TATTGGTATAAAGAAGGAAGCTGAAGAAAAAGAGAGAAAAGGAAAATG 138
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- web: www.genoscope.cns.fr)

- web: www.genoscope.cns.fr)

- betermination of this BAC-nd sequence was carried out as part of a collaboration with the BaC-nd sequence was carried out as part of a collaboration with the BaC-nd sequence was carried out as part of a collaboration of this BAC-nd sequence was carried out as part of a collaboration of the BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutooy oscogawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Store Genetic Strain y2; cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med buffalo.edu/drosophila_bac.htm.
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                                         79 TATTGGTATAAAGAAGGAAGCTGAAGAAAAAAAGAGAGACAAAAAGAGGAAAATAAAAG 138
                                                                   139 GGAATTGAAAAGGGAGAAAAAAGAAAAAGGGTAAGAAAGAATAAAAGAAAAAGATAA 198
                                                                                                                                                                         fruit fly.
Drosophila melanogaster
Bukaryota; Metava, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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//db.xref="taxon:7227"
/clone_lib="RRCT-98"
/clone="BACR13M18"
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Submitted (02-AUC-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKBN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp, Tel:81-45-503-911, Fax:81-45-503-9170)
Tel:81-45-503-911, Fax:81-45-503-9170)
Was generated during the R&D process and may have higher chance of colone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG031854.1 GI:16558727
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-005017.R.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AG031854 748 bp DNA linear GSS 01-NOV-2001 Pan troglodytes DNA, clone: PTB-005017.R, genomic survey sequence. AG031854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
0; Gaps
                                                                                                                                                                                                                                                       19 AAACATCTACATAAAAAAATAAAAACAGAAAAAAGAAAATGAAGAAAAGCCTGAGCCTGAGCCAGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (sites)
You'spana, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Wattanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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Toccki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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/clone_lib="PTB Chimpanzee Male BAC Library"
/ 26 c 76 g 8 t 28 others
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/db_xref="taxon:9598"
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15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laberto Submission of the Sequence of the Sequence of Submitted (02-JUN-1999) Genoscope - Centre National de Sequencege:

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                       JS7 bp DNA linear GSS 03-JUN-1999 BACR20W04 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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79 TATTGGTATAAAGAAGGAAGCTGAAGAAAAAAGAGAGGACAAAAGAGGAAAATAAAAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
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                                                      139 GGAATTGAAAAGGGAGAAAAAAGAAAAAGGGTTAAGAAAGAATTAAAAGAAAAAGGTTAA
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/db_xref="taxon:7227"
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/note="end : T7"
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
I-7-22 Suebiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mall:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS; GSS (genome survey sequence).

Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-018F21.F.

Pan troglodytes

Bac Library clone:PTB-018F21.F.

Pan troglodytes, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pan troglodytes DNA, clone: PTB-018F21.F, genomic survey sequence.
                                                                                                                          0; Gaps
                                               19 AAACATCTACATAAAAAATAAAAACAGAAAAAGAAAATGAAGAAAAGCCTGAGCCAGA
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
. 11 c 80 g 21 t 28 others
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Pred. No. 0.016;
0; Mismatches 89;
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-018F21.F"
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64.0%;
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Best Local Similarity 64.0°
Matches 158; Conservative
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Search completed: August 2, 2002, 16:53:17 Job time: 12278 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	<pre>Run on: August 2, 2002, 20:58:08 ; Search time 12674 Seconds</pre>	Title: US-08-973-363-13 Perfect score: 137 Sequence: 1 GATGGGATTGTTTCAGTGAAAAAAGAAAAGGAAAATAAGA 137	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 1797656 seqs, 10463268293 residues	Total number of hits satisfying chosen parameters: 3595312	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:* 1	
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SUMMARIES

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Query Match Length DB

No. Score Ma

Result

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/organism="Gallus gallus"
/db_xref="taxon:9031"
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                                                                                                                  Location/Qualifiers
 1 (bases 1 to 6872)
Griffiths, R. and Korn, R.M.
                                                                                                                                                                                                                                          /codon_start=1
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/gene="CHD-2"
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228. .5654
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chicken.
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                              AGAAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCTGGAGAAAAAAGAGAGACAAA 120
                         Gaps
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 Length 137;
                         Indels
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100.0%; Score 137; DB 6; 100.0%; Pred. No. 2.9e-16;
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Pred. No. 2.3e-13;
                                                                                                                                                                                                                                                                                                                                                    Patent: WO 9639505-A 12 12-DEC-1996;
Patent: WO 9639505-A 12 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Sequence 12 from Patent W09639505.
A58693
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:32644"
16 c 61 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.3%;
92.7%;
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                                                                                                                                                       121 AGAAAAGGAAAATAAGA 137
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             Best Local Similarity 100.
Matches 137; Conservative
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AF004397.1
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TITLE
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A CH11 gene is Z chromosome linked in the chicken Gallus domesticus Gene 197 (1-2), 225-229 (1997)
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LKQONVKGMNKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERIJ
AHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALIAKKRQARIDEYFSNQSSRAOSYPENYOKKKOPSYGGHESLELRDYQLNGLMTAHSWCKGNSCILADEMGLG
KTIQTISFLAYLFHEHGLYGFFLLRYDFLSTLTSWQRBIQTWAPQMNAVYLGDITSRN
MIRTHEWMHPQTKRLKFNILLTTYEILLKOKSFLGGLNWAFICVDEAHRLKNDDSLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGGKKOVNIYRLVTKGS
VEEDILERAKKKWULDHLVYQRMDTGKTVLHTGSTPSSSTPFWKEELSAIIKFGAEE
LEPEREGOEPQEMDIDEILKRAETRENEPGPLTVGDELLSGFKVANFSNMDEDDIE
LEPERNSTRINEEIIFBEGNERIJEEEERQKELEEITWLPFRRNCAKQISFNGSBGRRS
SRRYSGSDSDSITERKRFRKRGFRTIFPRENTKGFSDAEIRRFIKSYKKFGGPLERLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTLIDFKSNHRLLITGTPLONSLKELWSLLHFIMPEKFSSWEDFEEHGKGREYGYAS
LHKELEPFLLARVKROVEKSLPAKVEDILRMEMSALOKOYYKWILTRYKALSKGSKG
STSGFLNIMMELKKCONHCYLIKPPDDNEFYNKOEALGHLIRSGKLILLIRLR
STSGFLNIMMELKRCONHCYLIKPPDDNEFYNKOEALGHLIRSGKLILLIRLR
ERGNRVLIFSOXYVAMLDILAEYLKYROPPFQRLDGSIGGELRKOALDHFNAEGSEDFC
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RLAGAGNSKRRKTRNKKNKMKASKIKEEIKSDSSPQPSEKSDEDDEEEDNKDEIVSVK
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THVIRNPDVERLKETTNHDDSSRDSYSSDRHLSQYHDHHKDRHQGDAYKKSDSRKRPY
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/bortein_id="AAC60282.1"

/bortein_id="G01:2501846"

/t-anslation="WINGHSDEPSYRNSGESSRSDDDSGSAGGGGSSGSSBGSS
SQSGSSDSESGSSESGSGSESSESDTSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAV
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QVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDWGKEDDSNLLVGI
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SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
                                                                                                                                                                                                                                                       Criffiths, R. and Korn, R.M.
Direct Submitssion
Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 8QQ, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDDEDYDKRGSRRQATVNVSYKEAEETKTDSDDLLEVCGEDVPQTEEDEFET I EKFMD
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1223 c 1520 g 1683 t
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 6872)
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Pred. No. 2e-11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CHD-2"
/function="role in chromatin
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PRI 21-JUL-2001

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ACO21449 143079 bp DNA linear HTG 10-SEP-2000
Homo sapiens clone RPI1-58M12, WORKING DRAFT SEQUENCE, 10 unordered
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DE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell

Dive, Malnut Creek, CA 94598, USA

4 (bases 1 to 134365)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Submission Submission Submisted (21-JUJ-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 21, 2001 this sequence version replaced gi:14277267. Location/Qualifiers
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Mammalia; Butheria, Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 143079)
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143365)
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134365 bp DNA linear PRI 21-JUL-
Homo sapiens chromosome 5 clone CTD-2081117, complete sequence.
AC012624.6 GI:14993679
HTG.
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="5"
/clone="CTD-2082117"
40414 a 24497 c 25503 g 43951 t
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/db_xref="taxon:9606"
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Finishing Completed at Stanford Human Genome Center
Finishing Completed at Stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
Botimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 146.7kb). It is clipped at the overlap with AC012624.
The number of bases overlapped is 90404.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Bukarayota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101220)
DOB Joint Genome Institute and Stanford Human Genome Center.
Direct submission
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                                                                                    Ouery Match 60.9%; Score 83.4; DB 9; Length 101220; Best Local Similarity 80.3%; Pred. No. 6.4e.07; Matches 110; Conservative (), Mismatches 56; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       ACU92372 101220 bp DNA linear PRI 07-DEM
Homo sapiens chromosome 5 clone RP11-58M12, complete sequence
ACU92372
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18862 c 17827 g 30409 t
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/db_xref="taxon:9606"
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DOE Joint Genome Institute.
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VERSION
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 58_M_12
Center clone: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chamistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 139227 bases at least Q40
Consensus quality: 139227 bases at least Q20
Insert size: 144000; agarose fp
Insert size: 144779; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
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75509 92516: contig of 17008 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92517 92616: gap of 100 bp
92617 106409: contig of 13793 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38820: contig of 38820 bp in length
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40512 43279: contig of 2768 bp in length
43280 43379: gap of 100 bp
43380 46905: contig of 3526 bp in length
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38921 40411: contig of 1491 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
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46906 47005:
47006 518
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ACUUBS31 145659 bp DNA linear HTG 14-FEB-2001
Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE,
7 confered pieces.
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 117669 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAATTAAAACAGAAAG-AGACAGTGA 117727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 83.4; DB 2; Length 143079;
Pred. No. 6e-07;
0; Mismatches 26; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      906 others
                                                                                        /clone_lib="RPCI-11 Human Male BAC"
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43971 a 26246 c 26678 g 45278 t
                                                                                                                                                                                                                                         40512. .43279
/note="assembly_fragment"
43380. .46905
/note="assembly_fragment"
47006. .51830
/note="assembly_fragment"
51931. .62619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92617. .106409
/note="assembly_fragment"
106510. .143079
/note="assembly_fragment"
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75509. .92516
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                51931. .62619
/note="assembly_fragment"
                                                                                                                                                                                                  38921. .40411
/note="assembly_fragment"
1. .143079
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-58M12"
                                                                                                          1. .38820
/note="assembly_fragment
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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2 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                                             vector_side:left"
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80.3%;
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Best Local Similarity 80.3°
Matches 110; Conservative
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us-08-973-363-13.rge

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consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q40
Consensus quality: 180259 bases at least Q30
Consensus quality: 180259 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190346; sum-of-configs estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation
(unality coverage: 5.79 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a "working draft" sequence. It currently
consists of 33 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
                                                                                                                                                                                                                                                                Homo sapiens
Memorations Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammania; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 199446)
DOB Joint Genome Institute.
Sequencing of Human Chromosome 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Project Information
Center Project Name: 544799
Center clone name: RPCI-11_36012
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DOE Joint Genome Institute.
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40978:
41078:
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12560:
14611:
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HTGS_PHASE1
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                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                   TITLE
JOURNAL
  KEYWORDS
                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                        Consensus quality: 139128 bases at least Q40
Consensus quality: 14374 bases at least Q30
Estimated insert size: 14600; pulse fleid gel estimation
Cuality coverage: 6.27 in Q20 bases; pulse fleid gel estimation
Quality coverage: 6.27 in Q20 bases; pulse fleid gel estimation
Quality coverage: 6.27 in Q20 bases; pulse fleid gel estimation
Quality coverage: 6.27 in Q20 bases; pulse fleid gel estimation
Quality coverage: 6.27 in Q20 bases; pulse fleid gel estimation

* NOTE: This is a 'working draft' sequence. It currently
* are represented as runs of N. The order of the pieces
* 15 believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 55174 gap of unknown length
* 100975 ill3277 contig of fa173 bp in length
* 113228 118190: contig of tunknown length
* 11323 118190: contig of tunknown length
* 11329 113277: gap of unknown length
* 11329 113277: gap of unknown length
* 11329 119744: gap of unknown length
* 11329 119744: gap of unknown length
* 11329 113297: contig of 1404 bp in length
* 11329 113399 123399: gap of unknown length
* 123398 123399: gap of unknown length
* 123398 123399: gap of unknown length
* 123398 123399: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48345 AGAAAAACCTGAGCCAGATGTTTATATAAAGAACCAGAACCAGAAAAAGGGGAAGCAAA 48404
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26309 c 27580 g 48609 t 600 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1.145659
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="s"
/clone="crc-480811"
                                                                                          Project Information
Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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ACUV1382
276181 bp DNA linear HTG 03-JUL-2001
Homo sapiens chromosome 5 clone RP11-75H1, WORKING DRAFT SEQUENCE,
47 unordered pleces.
                                                                      Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek; CA 94598, USA
                                                                                                                                                                                                                                        Direct Submission

Direct Submission

Direct Submission

Direct (30-A001) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

On Aug 30, 2001 this sequence version replaced g1:15148108.

Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                              Direct Submission
Submitted (11-AGG-2001) DOE Joint Genome Institute, 2800 Mitchell
Burve, Walnut Creek, CA 94598, USA
4 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                                                      www.jgi.doe.gov
Frinshing Completed at Stanford Human Genome Center
www-shgc.stanford.ed
Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
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Pred. No. 5.6e-07;
0; Mismatches 26;
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a 42062 c 40933 g 64309
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/db_xref="taxon:9606"
/chromosome="5"
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1. 219258
                 2 (bases 1 to 219258)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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ilarity 80.3%;
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SHGC-103595 G57841
                                                      Direct Submission
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WI-5811 G04974
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                      gap of unknown length
1: contig of 10422 bp in length
1: gap of unknown length
2: contig of 6151 bp in length
3: gap of unknown length
3: gap of unknown length
                                                                                                                                                                                                                                                                             92891: gap of unknown length 102794: contrig of 9903 bp in length 102894: contrig of 9903 bp in length 110866: contrig of 7972 bp in length 110566: gap of unknown length 117571: contrig of 6605 bp in length 117671: gap of unknown length 123738: contrig of 6607 bp in length 139838: gap of unknown length 130583: contrig of 6745 bp in length 130583: contrig of 6745 bp in length
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/clone_lib="RPCI human BAC library 11"
35252 c 37061 g 60360 t 3202 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130683: gap of unknown length
141544: contig of 10861 bp in length
141644: gap of unknown length
169109: contig of 27465 bp in length
169209: gap of unknown length
193446: contig of 24237 bp in length.
                                                                                                                                                                f unknown length
g of 5563 bp in length
f unknown length
g of 7616 bp in length
                 unknown length
of 5982 bp in length
unknown length
of 5514 bp in length
                                                                                                                                                                                                                                          gap of unknown length
contig of 5180 bp in length
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/db_xref="taxon:9606"
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87512
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80.3%; Pred. No. 5.3e-07;
tive 0; Mismatches 26; Indels 1;
1990: gap of unknown length
40687: contig of 2887 bp in length
40689: contig of 348 bp in length
40689: contig of 348 bp in length
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46359: contig of 4802 bp in length
46359: contig of 4802 bp in length
46359: contig of 5468 bp in length
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46359: contig of 5468 bp in length
46350: contig of 6805 bp in length
4640: contig of 6805 bp in length
46527: contig of 6805 bp in length
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46627: contig of 6805 bp in length
46628: contig of 6805 bp in length
46629: gap of unknown length
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86859 a 51769 c 50026 g 82854 t 4673 others
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/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-75H1"
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Consensus quality: 229677 bases at least Q40
Consensus quality: 256163 bases at least Q20
Estimated insert size: 714820; agarose-fp estimation
Estimated insert size: 771581; sum-of-contigs estimation
Quality coverage: 8.52 in Q20 bases; agarose-fp estimation.
* NOTE: This is a 'working draft' sequence: It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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4327: contig of 1300 bp
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8728: gap of unknown 16
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8729: gap of unknown 16
8721: contig of 1222 bp
8721: contig of 1222 bp
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Web site: http://www.jg1.doe.gov
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Center Project Name: 435334
Center clone name: RPCI-11_75H1
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Submitted (14-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG 30-MAY-2000
                                                                                                                                                                                                                          Direct Submission
Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (bases 1 to 130030)
Waterston, R.H.
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Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 151,207 genomic DNA of 18p11.3
                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 130030) Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                               MO 63108, USA
On Jan 14, 1999 this sequence version replaced gi:3213108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57.4; DB 9; Length 130030;
Pred. No. 0.037;
0; Mismatches 46; Indels 0;
                                                         linear
                                                ncuvebby 130030 bp DNA linear Homo sapiens clone DJ0798C17, complete sequence. AC004889
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/ 25410 c 26567 g 39936 t
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HOMO Sapiens DNA, clone:RP11-872L6.
HOMO Sapiens
                                                                                                                                                                               The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .130030
Db 212053 AGAAAGGAGAATAAAA 212037
                                                                                       AC004889.1 GI:4156187
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Waterston, R.H.
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64.98;
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Best Local Similarity 64.9°
Matches 85; Conservative
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Published Only in DataBase (2000) In press
2 (bases 1 to 151207)
Hattori,M., Tshii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Hattori,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (05.JAN-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIREN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-855,
Japan (E-mall:hattori&gsc.riken.go.jp,
Pax:81-42-778-9923,
                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved
                                                                                                                                                On May 31, 2000 this sequence version replaced gi:6997422.
                                                                                                                                                                                                                                                                Sequencing vector: PCR products; 100% of reads Sequencing vector: PCR products; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 130559 bases at least Q40 Consensus quality: 140210 bases at least Q30 Consensus quality: 144545 bases at least Q20 Insert size: 147607; sum-of-contigs Quality coverage: 4.28x in Q20 bases; sum-of-contigs
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Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Contact: hattoridgsc.riken.go.jp
Center project Information
Center project name: HumDraft18
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ACO87566 231912 bp DNA linear HTG 10-JAN-2001
Mus musculus clone RP23-127H3, WORKING DRAFT SEQUENCE, 57 unordered
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DOE Joint Genome Institute.
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Live 0; Mismatches 49; Indels 0;
142919 144085: contig of 1167 bp in length 144186 145185: gap of 100 bp 145187 145286: contig of 100 bp in length 145187 145286: gap of 100 bp in length 14657 146756: gap of 100 bp in length 14657 146756: contig of 1370 bp in length 148757 148495: contig of 1739 bp in length 148757 14856: gap of 100 bp in length 148757 14856: gap of 100 bp in length 148757 148656: gap of 100 bp in length 148757 148156: contig of 1161 bp in length 149757 149165: gap of 100 bp
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HTG; HTGS_PHASE1; HTGS_DRAFT.
house mouse.
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Matches 86; Conservative
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Sequencing of Mouse

COMMENT

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gap of unknown length
contig of 13424 bp in length
gap of unknown length
contig of 8162 bp in length
gap of unknown length
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contig of 12007 bp in length
gap of unknown length
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contig of 5569 bp in length
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contig of 4552 bp in length
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contig of 7043 bp in length
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contig of 5715 bp in length
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contig of 9481 bp in length
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Consensus quality: 175115 bases at least Q30
Consensus quality: 175115 bases at least Q30
Consensus quality: 186307 bases at least Q30
Consensus quality: 186307 bases at least Q20
Estimated insert size: 226300; agarose-fp estimation
Estimated insert size: 226312; sum-of-contigs estimation
Quality coverage: 3.5 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 57 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                            Direct Submission
Submitted (10-JAN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
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1 (bases 1 to 152751)

Birran B., Linton.L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 4, clone RP11-257M8
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                     ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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40.1%; Score 55; DB 2; Length 231912;
Best Local Similarity 66.4%; Pred. No. 0.092;
Matches 79; Conservative 0; Mismatches 40; Indels 0,
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/clone="FR23-127H3"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing yearth; M13 M7815, 100% of reads Sequencing yearth; M13 M7815, 100% of reads Chemistry: Dyeterminator Big Dye; 100% of reads Assembly program: Phrap; version 0, 960731 Consensus quality: 146479 bases at least 040 Consensus quality: 146479 bases at least 030 Consensus quality: 160899 bases at least 030 Insert size: 151000; agarose-fp Insert size: 151000; agarose-fp Quality coverage: 4.9 in 020 bases; agarose-fp Quality coverage: 4.9 in 020 bases; sum-of-contigs
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EWRY cedex, FRANCE. (E-mail:

2 rue Gaston Cremieux, CP 5706, 91057 EWRY cedex, FRANCE. (E-mail:

seqref@qenoscope.cns.fr - Web: www.genoscope.cns.fr)

This STS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii. Zygosaccharomyces rouxii,

Saccharomyces Kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces
angueta, Debaryomyces hansenii var. hansenii, Pitchia sorbitophila,
Candida tropicalis and Varrowia lipolytica. Genomic inserts of 3 to
5 Kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.

Location/Qualifiers

irce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSOGJDL 969 bp DNA linear STS 10-JAN-2001 T3 end of clone ASOAA027H06 of library ASOAA from strain CLIB 533 of Saccharomyces bayanus, sequence tagged site.
                                                                                                                                                                                                    ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 969)

Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuharar,M., Bon,B., Brottier,P., Casaragodia,S.,
Bolotin-Fukuharar,M., Bon,B., Brottier,P., Casaragodia,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.,
Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of
FEBS Lett. 487 (1), 3-12 (2000)
11152876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 919)
Bon, E. Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P., Aigle, M. and Durrens, P.
Aigle, M. and Durrens, P.
Genomic Exploration of the Hemiascomycetous Yeasts: 5.
Saccharomyces bayanus var. uvarum
FEBS Lett. 447 (1), 37-41 (2000)
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                               Length 152751;
                                                                                                                                                                                                    ó
                                                                                                                                                                                                 47; Indels
                                                       1005 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Saccharomyces bayanus"
/strain="CLIB 533"
                                                                                                                                                  Score 53.8; DB 2;
Pred. No. 0.16;
0; Mismatches 47;
ture 109779. .152751
/note="assembly_fragment"
50931 a 26239 c 26351 g 48225 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL401455.1 GI:12159092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces bayanus.
Saccharomyces bayanus
                                                                                                                                               ch 39.3%;
1 Similarity 63.6%;
82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 969)
Genoscope.
                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 11671 AAAGAAAGA 11663
                                                                                                                                                                                                                                                                                                                                                                                                                                              129 AAAATAAGA 137
       misc_feature
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                                                    BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
CNSO6JDL
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBMED
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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Gaps
                                                                                                                                                                                                                                                         27 ACATAAAAAAATAAAAGCAGAAAAAAGAAAATGAAGAAAAAGATGAGCCAGAGATTGGTA 86
                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                        Length 969;
                                                                                                                                                                                                                                                                                                                                          87 TAAAGAAGGAAGCTGGAGAAAAAAGAGACAAAAAGAAAAGGAAAATAAGA 137
                                                                                                                              141 others
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                         35;

    .969
    /note="part of mitochondrial DNA"

                                                                                                                                                                                          Score 53.4; DB 11;
Pred. No. 0.48;
                                                                                                            /evidence=not_experimental
                                                                                                                                                                                                                         4; Mismatches
/variety="uvarum"
/db_xref="taxon:4931"
/clone="AsOBA07H06"
/clone=lib="ASOBA"
/note="end : T3"
                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: August 2, 2002, 20:59:53
Job time: 26834 sec
                                                                                                                                                                                          39.0%;
64.9%;
                                                                                                                                                                                          Query Match 39.0°
Best Local Similarity 64.9°
Matches 72; Conservative
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cancer

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P-PSDB; AAW08144.
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24-FEB-1998;
31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                       AAZ14372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
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                                                                                          A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAW08145) sequence are provided of a motif that is found spliced to the 3' end of chicken CHD-W clone CC14 (see also AAT42754). There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found as an insert in some CHD-1A clones
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                              1 GATGGGATTGTTTCAGTGAAACATCCACATAAAAAAATAAAAGCAGAAAAAAAGAAAATGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "base 52 disrupts the reading frame for
the translated amino acid sequence given
in Fig 7"
                                                                                                                                                                                               98.8%; Score 135.4; DB 18; Length 137; 99.3%; Pred. No. 1e-18; ive 0; Mismatches 1; Indels 0;
                                           Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                     Sequence 137 BP; 75 A; 10 C; 34 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                          Disclosure; Fig 7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                            AAT42752 standard; cDNA; 265 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken CHD-1A insert motif,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95GB-0011439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                             121 AGAAAAGGAAAATAAGA 137
                                                                                                                                                                                                                                                                                                                               121 agagaaggaaaataaga 137
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                   Conservative
Griffiths R, Tiwari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-043127/04
                  WPI; 1997-043127/04
                                                                                                                                                 (see also AAT42752)
                                                                                                                                                                                                         Local Similarity
nes 136; Conserv
                            P-PSDB; AAW08145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9639505-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus sp.
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                               AAT42752;
                                                                                                                                                                                                          Best Loca
Matches
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(AAW08144) sequence are provided of a motif that is found spliced to a proportion of chicken CHD-1A clones. The motif is inserted between bases 4327 and 4328 of the CHD-1A composite sequence (AAT42751). None of the 7 CHD-1 clones examined contained the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene; gene expression product; diagnosis; therapy; probe;
detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                  complete motif. There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found at the 3' end of the CHD-W clone CC14 (see also AAT42753).
                                                                                                                                                       A composite nucleotide sequence (AAT42752) and putative translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 265;
Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene expression product cDNA sequence SEQ ID NO:1841.
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Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA:
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Lesikowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 265 BP; 158 A; 16 C; 61 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

88.3%; Score 121; DB 18;
Best Local Similarity 92.7%; Pred. No. 7.6e-16;
Matches 127; Conservative 0; Mismatches 10:
                                                                                           Disclosure; Fig 7; 76pp; English
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98US-0072910.
98US-0075954.
98US-0080114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AGAAAAGGAAAATAAGA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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us-08-973-363-13.rng

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28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                  The present invention describes a library of human polynuclectides comprising the sequences given in AAZ1532 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product is encoded by one of the 5248 polynuclectide sequences given in AAZ12532 to AAZ1779. The coll of the folynuclectide sequences given in AAZ12532 to AAZ1779. The coll of polynuclectide sequences given in AAZ12532 to AAZ1779. The coll of polynociphisms. Polyneptides encoded by the polynuclectides and paping, tissue typing or profilling forensics, genetic analysis and detection of polynociphisms. Polypeptides encoded by the polynuclectides can be used for raising antibodies for experimental, diagnostic and bused for raising antibodies for experimental, diagnostic and necessary for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynuclectides of the invention are especially used in the defect and lung cancer. The polynuclectides can also be used to screen for peptide analogues and antagonists.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 ATGAGCCAGAGATTGGTATAAAGAAGGAAGCTGGAGAAAAAAAGAGAGACAAAAGAAAAGG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 38.1%; Score 52.2; DB 20; Length 300; Best Local Similarity 62.8%; Pred. No. 0.037; Matches 81; Conservative 0; Mismatches 48; Indels 0;
                                                                         Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 300 BP; 167 A; 37 C; 50 G; 46 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 8748.
                                                                                                                                                         Claim 1; Page 1076; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI88688 standard; cDNA; 392 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2001; 2001WO-US04927,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001 (first entry)
                      WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 AAAATAAGA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 aaaaaaaa 296
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that earthibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity activity immunomodulatory activity and activity activity immunomodulatory activity and activity and may be useful in the diagnosis and/or treamment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 CCAGAGATTGGTATAAAGAAGGAAGCTGGAGAAAAAAAGAGAGACAAAAGAAAAGGAAAAT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.1%; Score 52.2; DB 22; Length 392; Best Local Similarity 64.5%; Pred. No. 0.037; Matches 78; Conservative 0; Mismatches 43; Indels 0;
                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 8748; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 392 BP; 183 A; 53 C; 72 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 7768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI87708 standard; cDNA; 903 BP
                                                    Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2001; 2001WO-US04927.
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                                                                                                           WPI; 2001-514838/56.
(HYSE-) HYSEQ INC.
                                                                                                                                     P-PSDB; AAO08757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation.
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                                                                                                                                                                                                                                                       disorders
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09-APR-1999;
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                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 AAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCTGGAGAAAAAAAGAGAGACAAAAAAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
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                                                                                                                                                                      Claim 1; SEQ ID NO 7768; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein; gene therapy; vaccine; cancer; leukemia; autoimmune disease; allergy; inflammation; graft rejection; hyperproliferation; cardiovascular; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                       38.0%; Score 52; DB 22; Length 903; 62.1%; Pred. No. 0.041;
                                                                                                                                                                                                                                                                                                                                                                                                                             50; Indels
                                                                                                                                                                                                                                                                                                                                                                    Sequence 903 BP; 297 A; 208 C; 192 G; 199 T; 7 other;
                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding human secreted protein #24.
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o
                                                                  Tang YT, Liu C, Drmanac RT)
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        28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 aaaaaaaaaa 342
                                                                                         WPI; 2001-514838/56
                                                                                                                                                                                                                                                                                                                                  specification, but
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es 82; Conserv
                                            (HYSE-) HYSEQ INC
                                                                                                    P-PSDB; AAO07777
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Matches
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antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthhalmological; gene therapy; autoimmune disease; infection; hyperproliferative disorder; cardiovascular disorder; angiogenesis; cerebrovascular disorder; neurous system disorder; ocular disorder; wound healing; skin aging; food additive; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted protein; diagnosis; immunosuppressive; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 GATTGTTTCAGTGAAACATCCACATAAAAAATAAAAGCAGAAAAAAAGAAAATGAAGAAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to 26 secreted human proteins. The proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers (including leukemia), autoimmune diseases, allergies, inflammation, graft rejection, hyperproliferation, cardiovascular diseases inventionally critical limb ischemia and coronary disease) and any involving abnormal anglogenesis, neurodegeneration and/or
                                                                                                                                                                                                                                                  Nucleic acids encoding 47 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50;
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Pred. No. 0.041;
0; Mismatches 50
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                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 458-459; 525pp; English.
                                                                                                                              Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC93391 standard; cDNA; 2240
                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.0%;
ilarity 62.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0128702.
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                                                                                                                              Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nfectious diseases.
                                                                                                                                                                                     WPI; 2001-071148/08.
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11-JUN-1999;
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Best Local Simi
Matches 82;
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                                                                                                                           Rosen CA,
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The polynucleotide sequences given in AAC93364 to AAC93412 encode the human secreted proteins given in AAB51620 to AAB51668. AAB51669 to AAB51622 represent human secreted polypeptide sequences and proteins conditions. The polyneptide sequences and proteins have activities based on the present compologous to them, which are given in the exemplification of the present compologous to them, which are given in the exemplification of the present condition. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include:

CC offortability immunosupressive, antirheumatic; antiproliferative; criminal to antibacterial; virucide: fungicide; and be used to reuroprotective; antibacterial; virucide: fungicide; and be used to pervent, treat or ameliorate a medical condition; ne.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used to alphological condition. Disorders which are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardiovascular disorders, preferonsacular disorders, angiogenesis, nervous system disorders. Infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can also be used to aid wound healing and confisorders. The polypeptides can also be used to aid wound healing and companies, professes, to regenerate tissues and in chemotaxis. The pripartic confisorders and in chemotaxis. The present analyse be used as a food additive or preservative to primary tissues, to regenerate tissues and in chemotaxis. The pripartic configuration or supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The pripartic pripartic configuration or preservative to preservative t
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foetal abnormality; developmental abnormality; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.0%; Score 52; DB 21; Length 2240; ilarity 62.1%; Pred. No. 0.041; Conservative 0; Mismatches 50; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2240 BP; 532 A; 552 C; 623 G; 531 T; 2 other;
                                                                                                                                                                                                                                                                                       Claim 1; Page 443-444; 540pp; English.
                                                                                                               Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD08375 standard; cDNA; 2240 BP.
                                            (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
20-JAN-2000; 2000US-0177049.
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                                                                                                            Rosen CA, Ruben SM,
                                                                                                                                                      WPI; 2000-619225/59.
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es 82; Conserv
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Best Local S
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Abb08345-AAD08394 represent cDNAs corresponding to 50 human secreted protein agenes and AAE03989-AAE03947 represent the proteins they encode.

AAE03948-AAE03996 represent human secreted protein fragments or variants. The genes and their secreted protein fragments or variants. The genes and their secreted protein fragments or variants. The genes and their secreted protein for preventing the reacting or ameliarorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditions in the new genes. Specific uses are described for each of the conditioned developing products for the disponsis or treatment of proliferative disorders (e.g., proposer), dealed architis), inflammation, allowing an encological disorders (e.g., proposer), conditive disorders (e.g., promises), conditive disorders, encological disorders,
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immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; firlammetion; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; aspigoenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endedcrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; ss.
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/product= "Human secreted protein precursor"
1413..1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Mature human secreted protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein; diagnosis; autoimmune disease; ss; rheumatoid arthitis; hyperproliferative disorder; neoplasm; sunburn; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; skin aging; Allzhelmer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; chemotaxis; preservative; organ transplantation; tissue regeneration; food additive.
                                                                                                                                                 6 GATTGTTTCAGTGAAACATCCACATAAAAAATAAAAGCAGAAAAAAGAAAATGAAGAAA 65
                                                                                           Gaps
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                                                                                           ;
0
                                                     DB 22; Length 2240;
                                                                 0.041;
-hos 50; Indels
Sequence 2240 BP; 532 A; 552 C; 622 G; 531 T; 3 other;
                                                                      Pred. No. 0.04
0; Mismatches
                                                     Score 52;
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62.1%;
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angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to mainfrain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0; Mismatches
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PS Disclosure; SEQ ID NO 39473; 3071pp + Sequence Listing; Englis	Δ,
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rpeptides,

AXX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) and can be used in gene therapy and vaccine production. (I) and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and cample, they may be used to treat disorders associated with decreased cample, they may be used to treat disorders associated with decreased cuptained the activity of (I) by expression in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) proteins may be used to produce the secreted (I), by inserting the uncleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to provent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer mecastases of haematopoietic derived cells. AAK64703 cancers and cancer mecastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK5450 and AAM82169 crepresent sequences used in the exemplification of the present invention. Sequence 170 BP; 165 A; 0 C; 4 G; 1 T; 0 other;

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20000S-0229343.
20000S-0229345.
20000S-0229509.
20000S-0229503.
20000S-0229513.
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Query Match 37.8%; Score 51.8; DB 22; Length Best Local Similarity 64.7%; Pred. No. 0.044; Matches 77; Conservative 0; Mismatches 42; Indels
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18-APR-2000;
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Once: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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AAH33943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known, as colon cancer antigens. The colon cancer attigens have cytostatic activity and can be used in gene cancer attigens have cytostatic activity and can be used in the prevention, cancer attigens. The colon cancer attigens have cytostatic activity and be used in the prevention, cancer solon. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the patients own production of P. Additionally, N may be used to the proton cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell corporates the proteins. N and P can be used in the prevention, diagnosis and AABA7789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention. N.B. Pages 66 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 ITTCAGTGAAACATCCACATAAAAAATAAAAGCAGAAAAAAGAAAATGAAGAAAAAGAT 70
                                                                                                                                                                                                                                                                                                                               Human; colon cancer; colon cancer antigen; diagnosis; detection;
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tive 0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                         Human colon cancer antigen encoding cDNA SEQ ID NO:454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 2549; 9803pp; English.
                                                                                                                                                                           AAH33398 standard; cDNA; 2288 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM, Barash SC, Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0157137.
99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                     03-SEP-2001 (first entry)
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Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                   colorectal carcinoma; ss.
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                                        131 AATAAGA 137
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                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Conservative .

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AAI96873/c
ID AAI96873 standard; cDNA; 733
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es 71; Conserv
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                                                                                                                                                                     Homo sapiens
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Moore PA;
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                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosing, preventing and treating e.g. autoimmune, hyperproliferative, cardiovascular, and ocular diseases or disorders and microorganism infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 TTTCAGTGAAACATCCACATAAAAAATAAAAGCAGAAAAAAGAAAAAGAAAATGAAGAAAAAGAT 70
                            The present invention relates to 29 human secreted proteins. The invention is used to prevent autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, anglogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g.
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                                                                                                                                                                                                                                                                                                                                                                    DR,
                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid encoding 29 secreted proteins, for
                                                                                                                                                                                                                                                                                                                                                                    Ni J, Soppet DR
Komatsoulis GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                   Secreted protein; human; autoimmune; hyperproliferation; cardiovascular; cerebrovascular; infection; food; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2288 BP; 718 A; 467 C; 545 G; 558 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         corneal infection. Also used in food preparations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
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Pred. No. 0.045;
0; Mismatches 4
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Birse CE,
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                                                                                                                                      AAF72807 standard; DNA; 2288 BP
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Olsen HS,
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63.0%;
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Les 80; Conservative
                                                                                                                                                                                                 Secreted protein gene #9.
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Lafleur DW,
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                                                                                      2274 aaaaaaa 2280
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                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker
                                                                                                                                                                                                                                                  Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 CACATAAAAAAATAAAAGCAGAAAAAAGAAAATGAAGAAAAAGATGAGCCAGAGATTGGT 85
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                                                                                                                                                                                       Human neuroblastoma expressed polynucleotide SEQ ID NO 2948.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.4%; Score 51.2; DB 22;
66.4%; Pred. No. 0.059;
Live 0; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 2152; 2979pp; Japanese.
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BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2001; 2001WO-JP01629.
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PR 08-DEC-2000; 20000S-0251869.
PR 08-DEC-2000; 20000S-0251869.
PR 08-DEC-2000; 20000S-0251869.
PR 08-DEC-2000; 20000S-0251999.
PR 08-DEC-2000; 20000S-0251999.
PR 08-DEC-2000; 20000S-0251999.
PR 09-DEC-2000; 20000S-0251990.
PR 11-DEC-2000; 20000S-0254097.
PR 11-DEC-2000; 20000S-0254097.
PR M91; 2001-465557/50.
DR P-PSDB; AAD18190.
AXX WALLES and Parkinson's diseases and cancers - e.g. Proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers - e.g. Proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers - e.g. Proteins (AAU18194-AAU18194). and cDNA and genomic sequences encoding proteins (AAU18194-AAU18134), and cDNA and genomic sequences encoding cortisms (AAU18194-AAU18134), and cDNA and genomic sequences encoding proteins may contribute to diseases resulting from aberrant DNA corganisation and/or gene transcription. The sequences of the invention of chromatin organisation and/or gene transcription. The sequences of the invention of such as a listoners of DNA-binding proteins may be useful in treating disorders cancer as malignant diseases (e.g. cancer), autoformane disorders cancer and altabetes mellitus), rheumatic diseases (e.g. cancer), autoformane disorders carthitise), genetic abnormalities (e.g. cystic fibrosis), infections diseases (e.g. HIV) and neurological disorders (e.g. Alzheimer's cardinary of on one DNA-binding proteins may be useful in reating disorders cancer and in gene therapy. Associate for this patent cond not form part of the printed conception but was obtained in electronic format directly from WIPO Sequence 317 BP; 179 A; 36 C; 38 G; 47 T; 0 other;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: August 2, 2002, 16:53:17 ; Search time 8940.62 Seconds	(without alignments) 206.818 Million cell updates/sec	Title: US-08-973-363-13 Perfect score: 137 Sequence: 1 GATGGGATTGTTTCAGTGAAAAAAGAAAAGGAAAATAAGA 137	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 13736207 seqs, 6748477542 residues	Total number of hits satisfying chosen parameters: 27472414	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	<pre>Database : EST:* 1: em_estba:* 2: em_esthun:* 3: om_estinn:*</pre>	4: em_estn:. 5: em_estpo:* 6: em_estpo:* 7: em_estpo:*		15: em_gss_pin:* 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BF239967 601905170	AA748563 oa57c09.s	AI242163 qh81f02.x	. AA699918 zi61f12.s	BM015597 603641828	AI890775 wm95f11.x	AW387264 MR1-ST008	BE906261 601502247	BM415214 OP20286 M	BG548029 602575943	AW101322 sd77e07.y	BM480932 532632 MA	AG040706 Pan trod]	BM415207 OP20279 M	AL064007 Drosophil	AG040672 Pan trod1	AV685046 AV685046
SUMMARIES	ΩI	BF239967	AA748563	AI242163	AA699918	BM015597	AI890775	AW387264	BE906261	BM415214	BG548029	AW101322	BM480932	AG040706	BM415207	CNS006AG	AG040672	AV685046
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de	Query	66.1	6.09	6.09	6.09	6.09	59.1	53.9	42.5	42.2	41.0	40.9	40.6	40.3	40.3	40.1	40.1	40.1
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48888888888888888888888888888888888888	BE239967 601905170F1 NIH_MGC_54 Homo. BE239967.1 GI:11153890 EST. human. BER39967.1 GI:11153890 EST. humanalia: Eutheria: Primates Eukaryota: Metazoa; Chordata Mammalia: Eutheria: Primates I (bases 1 to 821) NIH-MGC http://mgc.nci.nih.go Mational Institutes of Healt Unpublished (1999) Institutes of Healt Unpublished (1999) Email: cgapbs-rémail.nih.gov Tissue Procurement: Arcc CDNA Library Preparation: C CON Library Preparation: C CON Sequence for D C C C C C C C C C C C C C C C C C C C
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Concact: nowart. acteausergy, Fn.D.

Email: cgapbs-remail.nih.gov
   Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
   Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
   Ph.D., Gerald Marti, M.D.
   CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
   Bonaldo, Ph.D.
   CDNA Library Arrayed by: Greg Lennon, Ph.D.
   DNA Sequencing by: Washington Dniversity Genome Sequencing Center
   Clone distribution: NCI-CGAP clone distribution information can be
   found through the I.M.A.G.E. Consortium/LLNL at:
   www.bio.lnl.gov/bbrp/image/image.html
   Insert Length: 1312 Std Error: 0.00
   Seq primer: -40ml3 fwd. EFT from Amersham
   High quality sequence stop: 282.
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="lthAGE:130907"
/clone="lthAGE:130907"
/clone="lthAGE:12GAP_GCBI"
/tissue_type="germinal center B cell"
/lab_host="bH108"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA748563
343 bp mRNA linear EST 27-JAN-1998 oa57c09:81 NCI_CGAP_GCB1 Homo sapiens CDNA clone INAGE:1309072 3's similar to SW:CHDI_MOUSE P40201 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN CHD-1. [1]; contains element L1 repetitive element;; mRNA
                                                                                                                                                                                                                                                                                                                          ó
                      (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 343)

NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

NCI-CGAP institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                        5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                Score 90.6; DB 10; Length 821;
Pred. No. 0.0047;
); Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
AA748563
AA748563.1 GI:2788521
                                                                                                                                                                                                                                                                     66.1%;
78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 AGAAAAGGAGAATAAAA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AGAAAAGGAAAATAAGA 137
                                                                                                                                                                                                                                                                                                                        Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .343
                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                     Query Match
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1...430
/organism="Homo sapiens"
/do_xref="taxon:9606"
/clone="IMAGE:1851099"
/clone="IMAGE:1851099"
/clone="IMAGE:1851099"
/clone="IMAGE:1851099"
/clone="IMAGE:1851099"
/clone="IMAGE:1851099"
/clone="IMAGE:1851099"
/clone="IMAGE:1851099"
/dev_stage="20 week-post conception fetus"
/
AI242163
430 bp mRNA linear EST 01-DEC-1998
qH81102.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA
clone IMAGE:1851099 3' similar to contains element LTR5 repetitive
element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 430)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1274 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality. sequence stop: 429.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AGAAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCTGGAGAAAAAAGAGAGACAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 83.4; DB 9; Length 343;
Pred. No. 0.054;
); Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                60.9%;
80.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 AGAAAGGAGAATAAAA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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TITLE
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us-08-973-363-13.rst

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BM015597 677 bp mRNA linear EST 30-OCT-2001 603641828F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5417887 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="organ: breast; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall, Cloned unidirectionally; oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AGAAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCTGGAGAAAAAAAGAGAGACAAA 120
                                                                                                                                                                                                                                    202 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAATTAAAACAGAAAG-AGACAGTGA 144
                                                                                                         1; Gaps
                                                                                                                                                 1 GATGGGATTGTTTCAGTGAACATCCACATAAAAAATAAAAGCAGAAAAAAGAAAATGA 60
                                                                                                                                                                                                                                                        143 AGAAAAACCTGAGCCAGATGTTATATAAAGAAGGAACCAGAAGAAAGGAAGCAAA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 60.9%; Score 83.4; DB 10; Length 677; Best Local Similarity 80.3%; Pred. No. 0.04; Marches 110; Conservative 0; Mismatches 26; Indels 1;
                                                             60.9%; Score 83.4; DB 9; Length 456; 80.3%; Pred. No. 0.047; Live 0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5417887"
/clone_lib="NIH_MGC_87"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BM015597
BM015597.1 GI:16529951
                                                                                                                                                                                                                                                                                                                     121 AGAAAAGGAAAATAAGA 137
                                                                                 Best Local Similarity 80.3%
Matches 110; Conservative
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                                                                  Query Match
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BM015597
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1. (bases I to 465)
Hillier,L., Allan,M.; Bowles;L., Dubuquer,T., Geisel,G., Jost,S., Krizman,D.; Kucaba,T.; Lacy,M., Le,N.; Lennon,G.; Marra,M., Martin,J.; Moore,B.; Schellenberg,K.; Steptoe,M.; Tan,F.; Theising,B.; Washite,Y.; Wylie,T.; Waterscon,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zi6ifi2.sl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA AA699918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
TMLS clone is available royalty-free through LLNL; contact the
TMLS clone is available royalty-free through LLNL; contact the
TMLGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 420.
LocatLon/Qualifiers
                                                                                                                                                                                                                61 AGAAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCTGGAGAAAAAAAGAGAGACAAA 120
                                                                                                                                                 1; Gaps
                                                                                                                                                                                        1 GATGGGATTGTTTCAGTGAAACATCCACATAAAAAATAAAAGCAGAAAAAAGAAAATGA 60
                                                                                                                                                                                                                                                                                                  constructed by Bento Soares and M.Fatima Bonaldo.
89 c 50 g 180 t
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/clone="lwAGB:435311"
/clone_lib="Soares_fetal_liver_spleen_INFLS_S1"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                    Query Match 60.9%; Score 83.4; DB 9; Length 430; Best Local Similarity 80.3%; Pred. No. 0.049; Matches 110; Conservative 6; Mismatches 26; Indels
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/db_xref="GDB:1335080"
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                                                                                                                                                                                                                                                                                                                                                          121 AGAAAAGGAAAATAAGA 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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DEFINITION AI890775/c

LOCUS

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

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782 bp mRNA linear EST 20-OCT-2000 601502247F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3904306 5', DE906261
                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR1&t2=MR1-ST0088-
101199-003-b09&t3=1999-11-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 27
High quality sequence start: 27
High quality sequence stop: 248.
                                             AW387264 249 bp mRNA linear EST 04-FEB-2000 MR1-ST0088-101199-003-b09 ST0088 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAATTAAAACAGAAAG-AGACAGTGA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 AGAAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAGAAGCAAAGGAAGCACA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73.8; DB 9; Length 249;
Pred. No. 0.95;
0; Mismatches 32; Indels
                                                                                                                                                                                                                                1 (bases 1 to 249)
HGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project Unpublished (1999)
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                                                                                                            AW387264.1 GI:6891923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 53.9%;
Best Local Similarity 75.9%;
Matches 104; Conservative
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                                                                                                                                                                              Homo sapiens
                                                                                        AW387264
                                                                                                                                                          human.
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ACCESSION
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                      AW387264/c
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TITLE
JOURNAL
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/organ's
/db_xxef="taxon:9606"
/clone="IMAGE:2443725"
/clone=lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1924 Std Error: 0.00
Seq primer: 40UP from Gibco
High quality sequence stop: 418.
Location/Qualifiers
1..547
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1 (bases 1 to 547)

NCI-GAP http://www.ncbi.nlm.nlh.gov/ncicgap.

NCI-GAP http://www.ncbi.nlm.nlh.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                  AI890775 547 bp mRNA linear EST 07-MAR-20C WAMSFILLX NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443725 3' similar to SW:CHDl_HUMAN 014646 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 ;, mRNA sequence.
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Pred. No. 0.086;
0; Mismatches 25; Indels
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AI890775.1 GI:5595939
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80.5%;
                                                                 121 AGAAAAGGAAAATAAGA 137
                                                                                                            209 AGAAAAGGAGAATAAAA 225
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Best Local S:
Matches 107;
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FEATURES

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human.

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/db_aref="taxon: Job6"
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/lab_ho
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 20). NIH-MGC http://mgc.nci.nih.gov/. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602575943F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703987 5', BG548029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: egapbs-rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be thtp://image.llnl.gov
http://image.llnl.gov e column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 ACATAAAAAATAAAAGCAGAAAAAAGAAAATGAAGAAAAAGATGAGCCAGAGATTGGTA 86
                                                                                                                                                                                                                                                                                                                                                               Query Match 42.2%; Score 57.8; DB 10; Length 973; Best Local Similarity 70.6%; Pred. No. 48; Matches 77; Conservative 0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 TAAAGAAGGAAGCTGGAGAAAAAAGAGAGAAAAGGAAAATAA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: LLCM1543 row: e column: 12
High quality sequence stop: 1.
Location/Qualifiers

    .200
    /organism="Homo sapiens"

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EST 28-JAN-2002
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Globodera pallida.
Globodera pallida
Bukaryota, Menazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.

1 (bases 1 to 973)
Heer,T., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
Mixed Stage EST's from Globodera pallida, the potato cyst nematode
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              973 bp mRNA linear EST 28-JAN-200 OP20286 Mixed Stage EST's from Globodera pallida, the potato cyst nematode Globodera pallida cDNA, mRNA sequence.
BM415214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 42.5%; Score 58.2; DB 10; Length 7 Best Local Similarity 68.1%; Pred: No. 47; Matches 81; Conservative 0; Mismatches 38; Indels
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Contact for the Biology of Nematode Parasitism
Canter for the Biology of Nematode Parasitism
Canter of the Biology of Nematode Parasitism
Canter for the Biology of New 27695, USA
Tall 919.515.6699
Fax: 919.515.9500
Email: warthogeunty.ncsu.edu
GTII-12000 R.HII_GTII-12_R.092.abl.
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BM415214.1 GI:18381669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Whyle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Beck, C., K., Ritter, E., Swaller, T., Gibbons, M., Parey, D., Harvey, N., Schurk, R., Materston, R. and Wilson, R., Var, Waterston, R. and Wilson, R., Waterston, R. and Wilson, R. Unpublished (1999)

L. Onpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
sap primer: -40RP from Gibco
High quality sequence stop: 128.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                              AW101322 230 bp mRNA linear EST 30-NOV-2001 sd77e07.yl Gm-c1009 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1009-445 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                              Gaps
                                                                                                78 AGATTGGTATAAAGAAGGAAGCTGGAGAAAAAAGAGAGAAAAAGAAAAGGAAAATA 134
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0
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/clone=id=wcms systems CLONE ID: Gm-c1009-445"
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     Length 200;
                                                   Indels
                                                 38;
  10;
  Score 56.2; DB 10
Pred. No. 1.5e+02;
                                                 0; Mismatches
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/organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW101322.1 GI:6071935
Query Match 41.0%;
Best Local Similarity 67.5%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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VERSION
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JOURNAL
COMMENT
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second-strand synthes is, the cDNA ends were 'polished' with Clone Pfu DNA polymerase, ligated to ECORI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the CDNA would be protected by their hemimethylated status. The CDNA constructs were size-fractionated with a 400bp cutoff, using a SizeSep 400 Spun column from Pharmacia. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that had been digested with EcoRI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with colNA inserts. This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 240)
Smith,T.P.L., Grose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
G.L., Heaton,M.P., Laegreeid,W.W., Rohrer,G.A., Chitko-Neckown,C.G.,
Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence evaluation of four pooled-tissue normalized bovine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ATGGGATTGTTTCAGTGAAACATCCACATAAAAAATAAAAGCAGAAAAAAGAAAATGAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              532632 MARC 4BOV Bos taurus cDNA 5', mRNA sequence. BM480932. GI:18531260 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56; DB 9;
Pred. No. 1.5e+02;
0; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: GTTTCCCAGTCACGACG
Plate: 2 row: A column: 7
Seq primer: ATTTAGGTGACACTATG.
Location/Qualifiers
1. 240
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PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GAAAAGGAAAATAAGA 137
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Mon Aug

us-08-973-363-13.rst

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/organism="Globodera pallida"
/db_xref="taxon.36090"
/clone_lib="Wiscox Stage EST's from Globodera pallida, the potato cyst nematode"
/note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G.pallida in lambda GT11 by Paul Burroughs, IRCR-Rothamsted " 25 others 189 c 81 g 609 t 25 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNSOU6AG 338 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR13M18 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchidae; Heteroderidae; Globodera.

1 (bases 1 to 940)
Heer,J.; Sosinski,B.; Pokrzywa,R.M.; Warry,A. and Opperman,C. Mixed Stage EST's from Globodera pallida, the potato cyst nematode Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                     940 bp mRNA linear EST 28-JAN-200 OP20279 Mixed Stage EST's from Globodera pallida, the potato cyst nematode Globodera pallida cDNA, mRNA sequence.
                                                                                                                                                                     Gaps
                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 GATTGGTATAAAGAAGGAAGCTGGAGAAAAAAAGAGAGACAAAAGGAAAAGGAAAATAAGA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 40.3%; Score 55.2; DB 10; Length 940; Best Local Similarity 65.2%; Pred. No. 1e+02; Matches 78; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                         36; Indels 0;
                                                                             Ouery Match

40.3%; Score 55.2; DB 12; Length 656;
Best Local Similarity 67.6%; Pred. No. 1.2e+02;
Matches 75; Conservative 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                   87 TAAAGAAGGAAGCTGGAGAAAAAAGAGAGACAAAAGGAAAAGGAAAATAAGA 137
                                                                                                                                                                                                                                                                                            Contact: Opperman, C
Center for the Biology of Nematode Parasitism
NC State University; IACR-Rothamsted
Campus Box 7616; Raleigh, NC 27695, USA
Tel: 919.515.6699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: warthog@unity.ncsu.edu
GT11-12PCN_R_H04_GT11-12_R_032.abl.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM415207
BM415207.1 GI:18381655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Globodera pallida.
Globodera pallida
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RTKEN), Genomic Sciences Center (555);
1-7-22 Suehiro-chou Tsurumi-ku, Vokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9110, Fax:81-45-503-9170,
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-018D03.R.
Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes DNA, clone: PTB-018D03.R, genomic survey sequence. AGG40706
AGG40706. GI:16569431
GSS; GSS (genome creek)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                   /note-"Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                 12 TICAGIGAAACAICCACATAAAAAATAAAAGCAGAAAAAAGAAAATGAAGAAAAAGAIG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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Gree can sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                        ó:
                                                                                                                                                                                                                                                                                   Query Match 40.6%; Score 55.6; DB 10; Length 240; Best Local Similarity 65.1%; Pred. No. 1.7e+02; Matches 82; Conservative 0; Mismatches 44; Indels 0.
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/clone_lib="PTB Chimpanzee Male BAC Library"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                           31 t
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1. .656
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-018D03.R"
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                        32 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
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a 19 c
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AGO40706
LOCUS
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SOURCE
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Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI disestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's and bw to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                   Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                       fruit fly.
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Buteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AAACATCCACATAAAAAATAAAAGCAGAAAAAAGAAAATGAAGAAAAAGATGAGCCAGA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 GATTGCTATAAAGAAGGAAGCTGGAGAAAAAAGAGAGACAAAAGAAAAGGAAAATAAGA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.1%; Score 55; DB 12; Length 338; 58.8%; Pred. No. 1.7e+02; tive 12; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/db.xref="Laxon:7227"
/clone_lib="RPCI-98"
/clone="BACRI3M18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 t
fly), genomic survey sequence.
AL064007
AL064007.1 GI:4944187
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9
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Matches 70; Conservative
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ORIGIN
                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
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Human colon cancer Mouse CHD-1 gene (Human digestive sy Human colorectal c

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Sequence:

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                  The chicken CHD-W gene (AAT42754) acting alone or in conjunction wit the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a
                                                                                                                                                                                                                  121 CATACAGGCTCTACTCCTTCAAGCTCAACACCTTTTAATAAGGAAGAGTTATCAGCAATT
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                                                                                                                                                                 Length 1316;
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Claim 1; Fig 8; 76pp; English.
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chromodomain-Helicase-DNA binding on the W chromosome; ss.
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         The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A - Anian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. Of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
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                                                                                                                                                                                                                                                                                                                                1 ATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAAGAAA 60
                                                                                                                                                                                                                                                                83.9%; Score 1104.6; DB 18; Length 6608; 90.4%; Pred. No. 2.3e-279; Live 0; Mismatches 125; Indels 0;
                                                                                                                                                                                                               Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
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961 CCTTCAGATCCAGAAGAAAGGAAAAGATATGTCATCCCATACCACACAAGCAGCTCAT 1020
                                                                                                                                                                                                          1021 TITGATATAGATIGGGGTAAAGAAGATGATICCAATCTGTTAATAGGCATCTATGAATAT 1080
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                                                                                                                                                                                                                                                               1081 GGTTATGGCAGTTGGGAAATGATAAAATGGATCCTGATCTCAGTTTGACACAGAAGATT 1140
                                                                                                901 GTGAATGCAAAGCTAGTCATTTCTCACGAAGAAGAGTTGGCACCATTGCATAAATCGATT 960
                                           841 AGAACAGGTGGTAGATTTGGGAAAGTTAAAGGCCCAACATTCCGAATAGCAGGAGTGCAG 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1261 GGCAATTCAAAGAGGAGAAAAACAAGAAGTAAGAAGAATAA 1301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding novel human diagnostic protein #21771.
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23-AUG-2000; 2000US-0649167.
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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving applyabiled in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical maging of sites expressing (II). (I) and (II) are useful for treating clasorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cappondates for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AASG4197-AASG4564 represent movel human conditing sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
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es 48; Indels
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Pred. No. 1.8e-
0; Mismatches
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Best Local Similarity 82.2%;
Matches 222; Conservative
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23-MAR-2000; 2000US-191637P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23; Length 6240;
                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
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49.9%; Pred. No. 5.8e-31;
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                                                                      Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9933 BP; 2711 A; 2468 C; 2538 G; 2216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                        Venter JC, Adams M,
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19-JUL-2001
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6109 gactccggtggcgactcggattacgagctgggctccgacggcagtggtgacgatggacga
                                                           cctcgcaagcgcgggcggccgaccatgaaggagaagatcaccggattcactgatgcggag
                                                                               ATTAGACGATTTATCAAGAGTTACAAGAAATTTGGTGGCCCAGTTGAAAGGTTAGATGCT
                                                                                                  6229 ttgcgtcgcttcattcgcagttacaaaaagtttcccgctcctccaccgcatggaggcc
                                                                                                                      ATAGCTAGAGATGCTGAGCTAGTTGATAAATCTGAAACAGACCTTAGACGTCTGGGAGAA
                                                                                                                                         atogoatgtgatgctgagctgcaggaaaagccactggcggaactgaagcgcctcggaagag
                                                                                                                                                             CITGTACATAATGGATGCATTAAGGCTTTAAATGATAATGACTTTGGTCAAGGAAGAACA
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                                                                                                                                                                                                                                                                                                                                             aagacacgcgccccggtcttcgacgtggattggggcatcgaggaggacacgaagctactg
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                                       607 AAACGTGGACGACCACGAACTATTCCCCGTGAAAACATTAAAGGATTTAGTGATGCAGAG
                                                                                                                                                                                                                                                                                                      ccgctcaacgagatcatgcccagcatgcccgaagagcgccagcaatggagcttcaatatc
                                                                                                                                                                                                     GGTGGTAGATTTGGGAAAGTTAAAGGCCCAACATTCCGAATA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGACTCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTG 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Altered telomere repeat binding factor 1 gene.
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/product= "A-TRF"
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Synthetic.
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The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, bown's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expressing A-TRF also have an increased life span in vitro, e.g. for expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAAGGAAAAGATATGTCATCCCATACCACACAAGCAGCTCATTTGATATAGATTGG 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.8%; Score 142.6; DB 19; Length 1311; Best Local Similarity 75.1%; Pred. No. 2.1e-27; Matches 178; Conservative 0; Mismatches 59; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human breast cancer expressed polynucleotide 18580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  breast cancer; cell marker; cytostatic;
                                                                                                                                                                                                                                                Van Steensel B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 110-111; 163pp; English.
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98WO-US02765
                                                               98US-0018628
97US-0800264
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                                                                                                                                                                                                                                                De Lange T,
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13-FEB-1998;
                                                                  04-FEB-1998;
                                                                                                13-FEB-1997;
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The invention relates to human breast cancer expressed polynucleotides (AAL057899) and methods of assessing whether a patient is affilicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and polynentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity.
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CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.3%; Score 122.8; DB 22; Length Best Local Similarity 79.7%; Pred. No. 2.8e-22; Matches 145; Conservative 0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 862 BP; 255 A; 139 C; 170 G; 292 T; 6 other;
                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                  Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
52.81
/*tag= a
/note= "bases 52-81 a
                                                                                                                                                                                                                                                        Claim 1; Page 1901; 3695pp; English.
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24-MAR-2000, 2000US-0192099.
29-MAR-2000, 2000US-0193480.
15-MAY-2000, 2000US-020530.
09-JUN-2000; 2000US-021315.
25-JUL-2000; 2000US-0220534.
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misc_difference
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                                                                                                                                              Lillie J,
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                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human breast cancer expressed polynucleotides (AALO7544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1045 GATGATTCCAATCTGTTAATAGGCATCTATGAATATGGTTATGGCAGTTGGGAAATGATA 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 985 AGATATGTCATCCCATACCACACCAAAGCAGCTCATTTTGATATAGATTGGGGTAAAGAA 1044
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                                                                                                                                                                                                                                                                                                               New peptide useful as a marker for the diagnosis of breast cancer
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                                                                                                                                                                                                                                     Lillie J, Xu Y, Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 3424; 3695pp; English.
                                                   ; 2000US-0176077.
; 2000US-0189167.
2000US-0193480.
; 2000US-0205230.
; 2000US-021315.
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Best Local Similarity 86.1%;
Matches 136; Conservative
                   10-JAN-2001; 2001WO-US00798
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14-MAR-2000; 2000US-0189167
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                                                   14-JAN-2000; 24-MAR-2000; 24-MAR-2000; 29-MAR-2000; 29-JUN-2000; 25-JUL-2000; 25-JUL-2000; 2
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Gaps

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DB 22; Length 862;

22-51 amino

ases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"

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1159 AAGAAACCCCAGGCTAAGCAGTTACAGACTCGTGCAGATTACCTCATTAAATTACTGAAT 1218
                                                                                                                                                                                                           Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology chic portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
"bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
                                                                                                                               Avian chromodomain-helicase-DNA binding genes determine sex in
birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.0%; Score 92.4; DB 18; 94.1%; Pred. No. 1.3e-14;
                                                                                                                                                                                                                                                                                                                                                                  Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHD-1A; CHD-W; W chromosome; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Great tit CHD-W gene fragment.
             (ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                94.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42759 standard; DNA; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
/note=
                                            Tiwari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-043127/04.
                                                                             WPI; 1997-043127/04
P-PSDB; AAW08147.
                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
misc_difference
                                            Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9639505-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT42759;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1159 AAGAAACCCCAGGCTAAGCAGTTACAGACTCGTGCAGATTACCTCATTAAATTACTGAAT 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromesome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                             Avian chromodomain-helicase-DNA binding genes determine sex in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 100.4; DB 18; Length 153;
Pred. No. 1.1e-16;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bird; sex determination; chromodomain-Helicase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss.

    used for sex determn. and to control sex of progeny

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                               Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.68;
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                                           96WO-GB01341
                                                                                                            (ISIS-) ISIS INNOVATION LTD
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                                                                            95GB-0011439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chick CHD-1A gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 99.0 ses 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..81
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                                                                                                                                               Tiwari
                                                                                                                                                                            WPI; 1997-043127/04.
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misc_difference
                                                                                                                                           Griffiths R,
                                           05-JUN-1996;
                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9639505-A1
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            12-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT42757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                birds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best

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Gaps

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Length 153; Indels

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AAA00010 to AAA02716 represent polynucleotides isolated from CDNA iltrarias constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell subsected of being cancerous, where detection of the differentially expressed gene product is correlated with a concerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting the polynucleotides can also be used as probes for defecting and mamplian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and commanian cell. The polynucleotides can also be used as probes for pre-metastatic or metastatic cancerous states, states, identification of pre-metastatic cancerous states, states, or negoniveness of cancer to therapy). This is particularly for breast cancer, obstrogen receptor-positive breast cancer, osetrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 tgaagtgtcancnagtgc---ncagatgaanttctatcacagantaaggttgtnaantt 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 GTTATCAGCAATTTTGAAGTTTGGTGCTGAGGAACTTTTTAAAGAACCTGAANNNGAAGA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 AGAGGAGCCTCAGGAGATGGATATAGATGAAATCCTGAAGGGNCTGAAAACTCGAGAAAA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 TGAGTCAGGCCCATTAACTGTAGGAGATGAGTTACTTTCACAGTTCAAGGTAGCTAACTT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 TICCAATAIGGAIGAAGAIGACATIGAATIGGAACCAGAAC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgcagcnatggangatgngtaactnntntaaaancntggnc 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 249 BP; 71 A; 31 C; 64 G; 61 T; 22 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.3%; Score 83.4; DB 21;
Best Local Similarity 60.6%; Pred. No. 3.7e-12;
Matches 134; Conservative 0; Mismatches 83;
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52..81
                          Claim 1; Page 480; 1097pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse CHD-1 gene (bases 3855-977).
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/note=
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misc_difference
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AMA
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Eschahard C, Giese K, Randazzo F, Kennedy GC, Pot LD, Kassam A;
Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide library used to determine cancerous states of mammalian cells – \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W Chromosome) gene (AAT42757), and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42755) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human colon cancer cell line polynucleotide sequence SEQ ID NO:1238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy, oestrogen receptor-negative breast cancer; therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                               in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.7%; Score 87.6; DB 18; Length 153; 91.2%; Pred. No. 2.4e-13; tive 0; Mismatches 9; Indels 0;
                                                       Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1219 AAAGACCTTGCAAGAAAGGAAGCACAGAGACTTGCTGGTGCA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA01247 standard; cDNA; 249 BP.
                                                                                                                                                        Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0085426.
98US-0085537.
98US-0085696.
98US-0105234.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 93; Conserv
P-PSDB; AAW08149.
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15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09958675-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Gaps

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2000US-0216880.
2000US-0217487.
2000US-0217496.
2000US-0218290.
2000US-0220963.
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2000US-0224519.
2000US-0225213.
2000US-0225214.
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2000US-0225267.
2000US-0225268.
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2000US-0241787
           07-JUL-2000; 2
11-JUL-2000; 2
14-JUL-2000; 2
26-JUL-2000; 2
26-JUL-2000; 2
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14-AUG-2000; 2
14-AUG-2000; 2
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14-AUG-2000;
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08-SEP-2000;
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02-OCT-2000;
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18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                              1159 AAGAAACCCCAGGCTAAGCAGTTACAGACTCGTGCAGATTACCTCATTAAATTACTGAAT 1218
                                                                                                                                                                                       Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT4275), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42755) the sea of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 aaaaaaccacaagcaaaacagttacagacccgtgcagactacctcatcaaactacttagc 111
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                        Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human digestive system antigen coding sequence SEQ ID NO: 1198.
                                                                                                                                                                                                                                                                                                                                                                        Score 67.4; DB 18; Length 153; Pred. No. 4.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                    21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1219 AAAGACCTTGCAAGAAAGGAAGCACAGAGACTTGCTGGTGC 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 153 BP; 61 A; 37 C; 27 G; 28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK88882 standard; cDNA; 421 BP
                                                                                                                                                                Claim 8; Fig 3; 76pp; English
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2000005-018664
2000005-0186350
200005-0189874
2000005-0198123
2000005-0205515
2000005-0205515
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                           (ISIS-) ISIS INNOVATION LTD
95GB-0011439
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Best Local Similarity 79.2<sup>3</sup>
Matches 80; Conservative
                                                   Tiwari B;
                                                                              WPI; 1997-043127/04
                                                                                             P-PSDB; AAW08146
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28-JUN-2000;
30-JUN-2000;
                                                     Griffiths R,
06-JUN-1995;
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1128 GACACAGAAGATTTTACCTGATGATCCAGATAAGAAACCCCAGGCTAAGCAGTTACAGAC 1187
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                                                                                                            DB 22; Length 421;
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                              61 T; 7 other;
                                                                                                         5.0%; Score 65.2; DB 2:
60.9%; Pred. No. 2.7e-07
iive 0; Mismatches 6:
                              A; 78 C; 127 G;
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2000US-018664
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2000US-021513
2000US-021513
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2000US-0225266.
2000US-0225267.
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2000US-0225270.
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                                                                                                            Query Match 5.08
Best Local Similarity 60.98
Matches 106; Conservative
                                  148
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                                  Sequence 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
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2000US-0249215.
2000US-0249216.
2000US-0249217.
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200005-0246527.
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2000US-0246523.
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2000US-0246525.
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2000US-0246613.
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2000US-0251856.
2000US-0251868.
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2000US-0249211.
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2000US-0249213.
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P-PSDB; AAM93109.
20 OCGT - 2000; 20 OCGT - 2000
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2000US-0229513.
2000US-0230437.
2000US-0230438.
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2000US-0237040.
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2000US-0240960
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2000US-0244617
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The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AAIS7547-AAIS7619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen coding sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1128 GACACAGAAGATTTTACCTGATGATCCAGATAAGAAACCCCAGGCTAAGCAGTTACAGAC 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1188 TCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAGAG 1247
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           2000US-0249209.
2000US-0249210.
2000US-0249211.
2000US-0249213.
2000US-0249214.
2000US-0249214.
2000US-0249215.
2000US-0249216.
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2000US-0249264.
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2000US-0249265.
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2000US-024929
2000US-024930
2000US-0250391
2000US-0251030
2000US-0251030
2000US-0251479
2000US-0251868
2000US-0251868
2000US-0251869
2000US-0251869
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Best Local Similarity 60.9
Matches 106; Conservative
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P-PSDB; AAM38625.
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                       17 - NOV - 2000;
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17-NOV-2000;
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229.2 17.4 643 10 BF611466 226.2 17.2 547 9 AIB90775 220.6 16.8 615 10 BF615108 219.8 16.7 1053 10 BM458124 217.4 16.5 438 9 BB830730 215.2 16.4 1028 10 RF895133	15.8 657 10 14.5 480 10 14.4 521 10 14.3 335 9	13.6 766 10 13.4 771 10 13.1 434 9 12.9 608 10	12.8 364 9 12.5 337 9 12.3 608 10	12.2 574 10 12.1 578 10	11.9 534	11.7 735 9 11.7 735 9 11.7 655 10		ALIGNMENTS		AK015218 Mus musculus adult male testis CDNA, RIKEN full-length enriched library, clone:4930428D05:chromodomain helicase DNA binding pro	1, full insert sequence. AK015218 AK015218.1 GI:12853470	HTC; CAP trapper. Mus musculus (strain:CS7BL/6J) adult m clone_lib:RIKEN full-length enriched m clone:493042BD05.	Pusa musical Amerazoa; Chordata; Craniata; Vertebrata; Euteleostomi Bukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu I (Sites).	High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)	10349636 2 (sites)	carninci, v. Snibata, v. Hayatak, v. Suganara, v. Snibatak, v. Ilitoh, M., Komo, H., Okazaki, Y. Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of Cap-trapper selected chokks to premare full-length char ilteration of cap-trapper selected chokks to	Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159	3 (Sites) Shibata,K., Itoh,M., Aizawa,K., Nagaok Konno,H., Akiyama,J., Nishi,K., Kitsun Gumi N Ishi V Nabamura Gumama	Jumin, N., 1911, Navamuru, J., Hazama Yamamoto, R., Matsumoto, H., Sakaguchi, S Fujiwake, S., Inoue, K., Togawa, Y., Izaw Yoneda, Y., Ishikawa, T., Ozawa, K., Tana	Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKBN integrated sequence analysis (RISA) system384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
c 19 22 c 20 22 c 20 22 21 21 22 21 23 211		28 30 31		302	386				RESULT 1	AKU15218 LOCUS DEFINITION	ACCESSION VERSION	KEYWORDS SOURCE	REFERENCE	TITLE JOURNAL	PUBMED REFERENCE	TITLE	JOURNAL MEDLINE PUBMED	AUTHORS		TITLE
4.5 Compugen Ltd.	Search time 8940.62 Seconds (without alignments) 1986.662 Million cell updates/sec	AATAAAGCAACAAAGGCTGC 1316		lues	:8: 27472414								ed by chance to have a of the result being printed, ore distribution.	-	Description	AK015218 Mus muscu AM997058 QV3-BN004 AU125712 AU125712	BC485663 602505962 BF427518 df89c11.y AL644594 AL644594	BB153.30 BB1253.50 ALG54479 ALG54479 BB461065 BB461065 AA41A472 vvc6412 c	AM46756 he21e07.x BF816895 MR2-CIO18 AL659353 AL659353	AL601246 DKFZp113J BB34922 BB34922 AL658477 AL658477 AW996787 QV3-BN004
GenCore version Copyright (c) 1993 - 2000 - nucleic search, using sw model	16:53:19 ; S	US-08-973-363-15 score: 1316 : ATTTATCGCCTAGTCACAAA	table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	13736207 segs, 6748477542 residues	er of hits satisfying chosen parameters	seq length: 0 seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	: EST:* 1: em_estba:* 2: em_esthum:*			ъ	12: qD_gss:* 13: em_gss_hun:* 14: em_gss_hun:* 15: em_gss_pln:* 16: em_gss_pln:*	No. is th greater t derived	SUMMARIES	ery tch Length DB ID	36.0 1811 11 34.9 686 9 33.3 866 9	31.6 765 10 31.2 633 10 29.9 645 9	29.4 622 9 27.2 660 9 26.0 482 9	25.2 609 9 23.9 459 10 22.3 593 9	268.6 20.4 430 9 AL601246 20.1 446 9 BB834922 237.2 18.0 642 9 AL65847 231.2 17.6 337 9 AW996787
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                                                                       Submitted (10-JUL 2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, RAL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-922, Please visit our web site (http://genome.gsc.riken.go.jp/) for
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SLPAKVEQILKMEWGALQKQYYKWILTRNYKALSKGSKGSYGGFLNIPMELKKCCNHC
YLIKPEDNNEFYNKQEALQKLITSKGKLILLDKLLIRLRERGNRVLIFSQWVEMLDIL
AEYLKYRQFPFQXLLOGSIKGELRKQALDHFNAEGSEDFCFLLSTRAGGLGINLASADT
VVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVTKGSVEEDILERAKKKWVLDHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                              The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="chromodomain helicase DNA binding protein 1 data source:MGD, source key:MGI:88393, evidence:ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="MGD:MGI:1907841"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAB29753.1"
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128. .1549
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                                                              FANTOM Consortium.
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Hart human CDAM Project (Ota.T., Wakamatsu,A., Ozawa.M., Ishli,S.,
HRI human CDAM Project (Ota.T., Wakamatsu,A., Ozawa.M., Ishli,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)

AL Unpublished (2000)
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Fax: 81-438-52-3952
Fax: 81-438-5
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 866)
Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Salto,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
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                                          GGCACCATTGCATAAATCGATTCCTTCAGATCCAGAAGAAAGGAAAAGATATGTCATCCC
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// Organism="Homo sapiens"
// Adv_rate="taxon:9606"
// Adv_rate="taxon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2707001
Email: aaimpson@ludwig.org.br
This aequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmil2.pl?ti=&t2=QV3-BN0047-150
400-152-c03&t3=2000-04-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 678
Location/Qualifiers
                            Bukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 686)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Garcia Correa, R., Werjovski-Almeida, S., Costa, F.P., Nagai, M.A., Ga Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Brunstein, A., Carvaho, A.F., Matsukuma, A., Bala, G. S., Simpson, D. H., M.J., Soares, F., Brentani, R. S., Bucher, P., Jongeneel, C. V., O'Hare Simpson, A.J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 TCCATCTCAGAAAGAAAACGACCAAAAAAACGTGGACGACCACGAACTATTCC-CCGTGA 638
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Local Similarity 83.3%; Pred No. 4.9e-80;
18es 546; Conservative 0; Mismatches 108; Indels 2.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 765)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1990)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    989 ATGTCATCCCATACCACACCAAAGCAGCTCATTTTGATATAGATTGGGGTAAAGAAGATG 1048
                                                                                                                                                                                                                                                                                                                         1049 ATTCCAATCTGTTAATAGGCATCTATGAATATGGTTATGGCAGTTGGGAAATGATAAAAA 1108
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1378 row: 1 column: 15
High quality sequence stop: 593.
                                                                                                                                                            181 AGGGTCCAACATCCGAATATCAGGAGTACAGGTGAATGCCAAACTAGTCATCTCCCATG 240
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/clone_Inb="NH MGC_77"
/clone_Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' and
sequence: 5'-CACGGCGCATTGGCC_3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGCATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert B = A,
C, or G and N = A, C, G, or T). Average insert B = B,
C, or G and N = A, C, G, or T). Average insert B
by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
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clone IMAGE:3746325 5' similar to TR:042142 042142
CHROMO-HELICASE-DNA-BINDING ON THE Z CHROMOSOME PROTEIN. ;,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 415.8; DB 10;
Pred. No. 1.5e-71;
0; Mismatches 104;
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82.3%;
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Mon Aug

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AL644594 G45 bp mRNA linear EST 07-NOV-2001 AL644594 XGC-egg Silurana tropicalis cDNA clone LlE1d12 5', mRNA
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         998 CATACCACACCAAAGCAGCTCATTTTGATATAGATTGGGGTAAAGAAGATGGTTCCAATC 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           758 CTGAAACAGACCTTAGACGTCTGGGAGAACTTGTACATAATGGATGCATTAAGGCTTTAA 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 CATTICGIATCTCAGGGGTGCAAGTGAATGCAAAGTTGGTCAGTTCCCATGAAGAAGAG 478
    182 AAAATATTAAAGGCTTTAGTGATGCTGAGATAAGGAGGTTTATTAAAAGCTACAAAAAGT 241
                                                                                 698 TIGGIGGCCCAGTIGAAAGGITAGAIGCTATAGCTAGAGAIGCTGAGCTAGTIGATAAAI 757
                                                                                                                            818 ATGATAATGACTTTGGTCAAGGAAGAACAGGTGGTAGATTTGGGAAAGTTAAAAGGCCCAA 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              878 CATTCCGAATAGCAGGAGTGCAGGTGAATGCAAAGCTAGTCATTTCTCACGAAGAGAGT 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           938 TGGCACCATTGCATAAATCGATTCCTTCAGATCCAGAAGAAAGGAAAAGATATGTCATCC 997
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Emall: trop@sanger.ac.uk
Sanger Kenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: LiEld12.plc
Sequencing primer: PlC
This sequence is from a Xenopus Gene Collection (XGC) library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sangar Xenopus tropicalis EST project 2001 (10_2001) (Unpublished (2001) Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Silurana tropicalis"
/db_xxef="taxon:8364"
/clone="LiBid12"
/clone=lib="XGC-egg"
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Location/Qualifiers
1. .645
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AL644594.1 GI:16796719
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1 (bases 1 to 645)
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TITLE
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//Uydairan_Acaropus_Acarots
//Clone=lib="Acaropus_Base"
//Clone=lib="Xecopus_Base"
//Clone=lib="Xecopus_Base"
//Lissue_type="cocyte (stages 5 and 6)"
//Lib_host="rop-10 f"
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Annura; Mesobatrachia; Pipoidea; Pipidae; Kanopodinae; Kanopus.

1 (Dases 1 to 633)

1 (Dases 1 to 633)

1 (Martin J., Wylle, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., Mccann, R., Waterston, R. and Wilson, R.

Washu Xenopus EST project, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by:
Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
below when ordering this clone: Source lab clone id - xinnoc004f22
Seq primer: -40RP from Gibco
High quality sequence stop: 408.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contract: Sandy Clifton, Ph.D.
WashU Kenopus Est project, 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
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a 114 c
African clawed frog.
Xenopus laevis
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Matches 501; Conservative
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Arakwa,Tr., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishil,Y., Ito,M., Kawai,J., Konno,H., Kouda,Okazaki,Y., Okido,T., Salto,R., Sakai,K., Sano,H., Sasaki,D., Shibaga,K., Shinagaw,A., Shiraki,T., Soqabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

FIREN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jun 29, 2000 this sequence version replaced g1:8811286.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB155356 RIKEN full-length enriched, 16 days neonate thymus Musmusculus cDNA clone A130024116 3' similar to L10410 Mouse DNA binding protein (CHD-1) mRNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                311 TATCCCATGCCACACCAAAGCTGCTCATTTTGATATTGACTGGGGCAAAGAAGATGACTC 370
                                                                   693 GAAATTTGGTGGCCCAGTTGAAAGGTTAGATGCTATAGCTAGAGATGCTGAGCTAGTTGA 752
                                                                                                                                    753 TAAATCTGAAACAGACCTTAGACGTCTGGGAGAACTTGTACATAATGGATGCATTAAGGC 812
                                   Gaps
                                                                                      14 GAAAGTITGGCGGGACCTCTAGAAGGTTAGATGCAATAGCCCGAGATGCTGAGATGGTGGA 73
                                                                                                                                                          191 ACCAACATTCCGTATCTCAGGGGTGCAAGTGCGAAGTTGGTCAGTTCTCATGAAGA
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                                                                                                                                                                                                        813 TTTAAATGATAATGACTTTGGTCAAGGAAGAACAGGTGGTAGATTTGGGAAAGTTAAAGG
                                                                                                                                                                                                                                                                         873 CCCAACATTCCGAATAGCAGGAGTGCAGGTGAATGCAAAGCTAGTCATTTCTCACGAAGA
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                                 0; Mismatches
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29.9%;
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                                 Matches 486; Conservative
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Tel: 81-45-503-9222
Fax: 8
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(SGC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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/db_xref="taxon:10090"
/clone="A130024L16"
/clone="hallo"RIKEN full-length enriched, 16 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
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Pred. No. 5.9e-66;
0; Mismatches 138;
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Best Local Similarity 77.6%;
Matches 481; Conservative
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/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="tgaso44co6"
/clone=lib="xcc-qastrula"
/clone_lib="xcc-qastrula"
/dev_stage="gastrula" (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XLJ-blue"
/note="Vector: pCS107; Site_1: BcoRi; Site_2: Not1; cDNA
was oligo dT primed from Sug of poly 4+ RNA from stages
lo-13 gastrulae. ECORI-Not1 cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and Not1 at the 3'
end. ROSIO7 with EcoRI at the 5' end and Not1 at the 3'
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                240 TCTGGAGTCCAAGTGAATGCCAAGCTGGTCATTGCCCATGAGGATGAGGATCCCTCTG 299
          649 GGATTTAGTGATGCAGAGTTAGACGATTTATCAAGAGTTACAAGAAATTTGGTGGTGGCCCA 708
                                                                         709 GITGAAAGGTIAGAIGCIATAGCIAGAGAIGCIGAGCIAGIIGAIAAAICIGAAACAGAC 768
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Sanger Xanopus tropicalis EST project 2001
Sanger Xanopus tropicalis EST project 2001
TROPICALIS_ESTORE.ID: TGAS044c06.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
                               Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Uppublished (2001)
Contact: Huckle E
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Silurana tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Gaps
                                                                                                                                                                                                                                               Length 622;
                                                                                                                                                                                                                                        29.4%; Score 387.2; DB 9; Length 6
80.0%; Pred. No. 5.9e-66;
Live 0; Mismatches 118; Indels
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115 c
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482 bp mRNA linear EST 04-AUG-1997 nowles Solter mouse 2 cell Mus musculus cDNA clone 5' similar to 9b:X66028 M.musculus mRNA KYBP (MOUSE);
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
980 GGAAAAGATATGTCATCCCATACCACACCAAAGCAGCTCATTTGATATAGATTGGGGTA 1039
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IMAGE:778871 5' similar to gb:X6
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                                                                                                                                                           Analmaitai Louinella, November, Louinela, Louinela, Hanagaki, T., Hara, A., Hanagaki, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hanando, K., Horil, F., Ishi, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinaqawa, A., Shinaqawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Muramatsu, M., and Hayashizaki, Y., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS, (Arakawa, T., et al. 2001)
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Atlastue_type="12 days embryo"
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Anote="site_1: SalI; Site_2: BamHI; cDNA library was proper of Genome Exploration Research Group in Riken Genomic Science Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 1757-1771 (2000) (11), 
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URL:http://genome-gs.gr.riken.go.jp,
URL:http://genome-gs.gr.riken.go.jp,
Carninci.p., Shibata,Y. Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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Normalization and subtraction of cap-trapper-selected cDNAs to
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A.S., Rawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
On Jul 21, 2000 this sequence version replaced gi:9356558.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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/db_xref="taxon:10090"
/clone="D130070B13"
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us-08-973-363-15.rst

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Matches 373; Conservative
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Unpublished (1997)
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                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:471727
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 368.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-*Organ: embryo; Vector: pBluescribe (modified); Site_1: MluT; Site_2: SalT; Cloned unidirectionally framRNA prepared from 13,500 2-cell stage embryos. Prim SalI(dT); 5'-CGGTCGACCGTGACCGTTTTTTTTTTTTTTT'. CD Were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NBB). Average insert size: 1.2 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 GTGCTGAGGAACTTTTAAAGAACCTGAANNNGAAGAAGAGGGGGCCTCAGGAGATGGATA 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 TTGAATTGGAACCAGAACAAAATCTAAGAAACTGGGAAGAAATCATTCCAGAAGTTCAGT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TIGAATIGGAACCIGAAAGAAATICAAAGAACIGGGAGGAGATCATICCAGAAGAGCAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 GGCGACGAATAGAGGGGNNGGAAAGACAAAAAGAACTTGAAGAAATATATATGCTTCCAA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491 GAATGAGAAACTGTGCAAAACAGATCAGCTTTAATGGAAATGAAGGGAGATGCAGTAGGA 550
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Materston,R.
                                                                         The Wash). HiMI Mouse EST Project
Uppublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.0%; Score 342.2; DB 9; Length 482; llarity 81.5%; Pred. No. 3.7e-57; Conservative 0; Mismatches 89; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib-"knowles Solter mouse 2 cell"
/issue_type-"embryo"
/dev_stage-"2-cell"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                      /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:778871"
                                                                                                                                                                                                                                                                                                                                                                                       /strain="B6D2 F1/J
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Matches 392; Conserve
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heled).x1 NCL_CGAP_CML1 Homo sapiens CDNA clone IMAGE:2919684 3' similar to SW:CHDL_HUMAN 014646 CHROMODOMAIN-HELICASE-DNA-BINDING PROFIEIN 1; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Sequencing Center
Clone distribution: NI-CGAP Clone distribution information can be
Clone distribution: NI-CGAP. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 380.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Emall. cgapbs-remail.nh gov
Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,
Michhael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Iro. CoNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone='IMAGE:2919684"
/clone=lib="KCLGAP_CML1"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL rearrangement positive, includes both chronic phase and myeloid blast crisis"
/lab_host="BH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 60.9). NOI.-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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AW467566.1 GI:7037672
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Gaps

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AL659353 XGC-neurula Silurana tropicalis cDNA clone TNeu045e20 5',
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/clone_lib="XGC-neurula"
/dev_stage="neurula"
/dev_stage="neurula"
/lab_host="Becherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from Sig of poly A+ RNA from neurula. EcoRI NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                 GACACCACAGGGAAAACTGTACTACATACAGGCTCTACTACTCCTTCAAGCTCAACACCTTTT 156
                                                            337 GTAGCTAACTTTTCCAATATGGATGAAGATGACATTGAATTGGAACCAGAACAAAATCTA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 AGAAACTGGGAAGAAATCATTCCAGAAGTTCAGTGGCGACGAATAGAGGGGNNGGAAAGA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAAAAGAACTTGAAGAAATATATATGCTTCCAAGAATGAGAAACTGTGCAAAACAGATC 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu045e20.sp6
Sequencing primer. SP6
This sequence is from a Xenopus Gene Collection (XGC) library
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Xenopodinae; Silurana.

1 (bases 1 to 59)

Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (10_2001)

Contact: Huckle E
Sanger Centre
                                                                                                                                                 277 ACTCGAGAAAATGAGTCAGGCCCATTAACTGTAGGAGATGAGTTACTTTCACAGTTCAAG
                                                                                                                                                                                                                                                                                                                            157 AATAAGGAAGATTATCAGCAATTTTGAAGTTTGGTGCTGAGGAACTTTTTAAAGAACCT
                                                                                                                                                                                                                  GAANNNGAAGAAGAAGCCTCAGGAGATGGATATAGATGAAATCCTGAAGAGGNCTGAA
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92;
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/organism="Silurana tropicalis"
/db_xref="taxon:8364"
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Mismatches
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Location/Qualifiers
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AL659353
AL659353.1 GI:17672995
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366; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 459;
Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-CI0184-081200-002-h01&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                   BF816895 459 bp mRNA linear EST 13-JAN-2001
MR3-CI0184-081200-002-h01 CI0184 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Frudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                          360
                                                                                                                                                                                              361 GAAGATGACATTGAATTGGAACCAGAACAAAATCTAAGAAACTGGGAAGAAATCATTCCA 420
                                                                                                                                                 98
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                                                                                                                                                                                                                    GAGATGGATATAGATGAAATCCTGAAGAGGNCTGAAACTCGAGAAAATGAGTCAGGCCCA
                                                                                                         301 TTAACTGTAGGAGATGAGTTACTTTCACAGTTCAAGGTAGCTAACTTTTCCAATATGGAT
                                                                                                                               Score 314.4; DB 10; Length 459; Pred. No. 1e-51;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="c10184"
/dev_stage="Adult"
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Akinura, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Havaka, T., Miradok, T., Inchani, K., Ishi, Hayakasu, N., Hiramcho, K., Hiradoka, T., Hirzane, T., Inchani, K., Ishi, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Mishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinaqawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku, Ashira, S., Tanaka, T., Tomaru, A., Togavu, Matahiki, A., Yasunishi, A., Wuramatsu, M., and Hayashizaki, Y.
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BB834922 RIKEN full-length enriched, mammary gland RCB-0527
Jyg-WC(B) EDNA Mus musculus CDNA clone G930033321 3', mRNA
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Akimura,I., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,I.,
                                                                                                                                                                          Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                             922 TCTCACGAAGAAGAGTTGGCACCATTGCATAAATCGATTCCTTCAGATCCAGAAGAAGG 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 AAGCAGTATACTATCCCATGCCACACAAGGCAGCTCATTTTGATATAGACTGGGGCAAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 AAACCACAAGCAAAAACAGTTGCAGACCCGTGCAGACTACCTCATCAATTACTTAGTAGA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 20.4%; Score 268.6; DB 9; Length 430; Local Similarity 82.2%; Pred. No. 9.1e-43; hes 323; Conservative 0; Mismatches 64; Indels 6;
     1. 430
/organism="Homo sapiens"
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/clone="DkFzp313J1040"
/clone="Lb="131" (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1282 ACAAGAAGTAAGAAGAATAAAGCAACAAAGGCT 1314
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OKFZp313J1040_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DKFZp313J1040 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Bukarayota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 430)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and
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No s1 sequence available.

This clone (DKF2913J1046) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                 1011 AGCAGCTCATTTTGATATAGATTGGGGTAAAGAAGATGATTCCAATCTGTTAATAGGCAT 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1071 CTATGAATATGGTTATGGCAGTTGGGAAATGATAAAAATGGATCCTGATCTCAGTTTGAC 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1131 ACAGAAGATTTTACCTGATGATCCAGATAAGAACCCCAGGCTAAGCAGTTACAGACTCG 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1191 TGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAGAGACT 1250
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                                                                                                                                                                                                                                                                                                                                                                                                                             293 AGCTGACTACCTCATTAAACTTCTCAATAAAGATCTGCTTAGGAAAGAAGCACAAAGACT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 891 AGGAGTGCAGGTGAATGCAAAGCTAGTCATTTCTCACGAAGAAGAGTTGGCACCATTGCA 950
                                                                                                                                                                                                                           353 ACAGAAGATTTTACCAGATGATCCAGATAAGAAGCCCCAAGCCAAGCAGCTACAGACCAG 294
                                                                                                                                                      0; Gaps
                                                                                                  Score 293.8; DB 9; Length 593;
Pred. No. 1.1e-47;
0; Mismatches 82; Indels 0
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AL601246.1 GI:15164752
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  134 c
                                                                                                                            Best Local Similarity 80.79
Matches 343; Conservative
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Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninoi,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected conns to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. .10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tzawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
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Hayashizaki,Y.
RIKBN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
.Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-22 Suebliro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encyclopedia: real-time sequence clustering for construction of norredundant cNNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA"
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/99 c 108 g 100 t
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Pred. No. 5e-42;
0; Mismatches 102; Indels 1
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Best Local Similarity 76.6's
Matches 337; Conservative
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1256 GTGCAGGCAATTCAAAGAGG 1275

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Db 427 GTTCGGAGGTTCAAAGAGG 446
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Search completed: August 2, 2002, 16:53:29 Job time: 12290 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 1100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched:

US-08-973-363-15

Perfect score: Scoring table:

Run on:

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Database :

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Query Score Match Length DB Result

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         Length 1316;
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       Score 1310; DB 6; I
Pred. No. 2.5e-284;
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99.5%; Scor.
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Best Local Simi
Matches 1316;
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IKKELWSLLHFINPEKFSSWEDFEEEHGKGREFGYASLHKELEPFLLRRVKKDVEKSSP
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RAETRENESGLITVGDELLSQFKVANFSNMDEDDIELEPEQNLRNWEEIIPEVQWRRI
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helicase DNA binding
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1 (bases 1 to 2943)
Fridolfsson, A. K. and Ellegren, H.
Molecular evolution of the avian CHDl genes on the Z and W sex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTACCTGATGATCCAGATAAGAAACCCCAGGCTAAGCAGTTACAGACTCGTGCAGATTAC 1200
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Fridolfsson,A.-K. and Ellegren,H.
Direct Submission
Submitted (30-AUG-1999) Department of Evolutionary Biology,
Evolutionary Biology Centre, Uppsala University, Norbyvagen
Uppsala S-75236, Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1261 GGCAATTCAAAGAGGAGAAAAAACAAGAAGTAAGAAGAAGAATAAAGCAACAAGGCTGC 1316
TTTGATAGATTGGGGTAAAGAAGATGATTCCAATCTGTTAATAGGCATCTATGAATAT
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EEEERQKELEEIYMLPRMRNCAKQISFNGNEGRCSRSRRYSGSDSDSISERKRPKKRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661 GCAGAGATTAGACGATTATCAAGAGTTACAAGAAATTTGGTGGCCCAGTTGAAAGGTTA 720
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                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                   1 ATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAAGAAA 60
                                                                                                                                                                                     87.1%; Score 1146.8; DB 5; Length 2943; 98.9%; Pred. No. 1.1e-247; Live 0; Mismatches 13; Indels 0;
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Matches 1151; Conservative
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linear PAT 06-MAR-1998
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Griffiths,R. and Tiwari,B.
AVIAN GHDG GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1021 TITGATATAGATIGGGGTAAAGAAGAIGATTCCAATCTGTTAATAGGCATCTAIGAATAT.1080
                                                                                                                                                    1081 GGTTATGGCAGTTGGGAAATGATAAAAATGGATCCTGATCTCAGTTTGACACAGAAGATT 1140
                                                                                                                                                                                                                      3123 TTGAAGTTTGGTGCTGAGGAACTCTTTAAAGAACCTGAAGGAGAAGAAGAAGAGGAGCCCCAG 3182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AAGATGGTGTTAGATCATTTAGTGATTCAGAGAATGGACACCACAGGGAAAACTGTACTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CATACAGGCTCTACTCCTTCAAGCTCAACACCTTTTAATAAGGAAGAGTTATCAGCAATT 180
901 GTGAATGCAAAGCTAGTCATTTCTCACGAAGAAGAGTTGGCACCATTGCATAAATCGATT 960
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                                                                                                                                                                                                                                                                                                                                                                                             DNA
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 from Patent W09639505.
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/db_xref="taxon:32644"
1207 c 1459 g 1655
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SQSGSSDESEGSGSESCETSREKKQVQARPRADGESFWRSSPSILAVQRSAV
IKKQQQQQKAASDGSGEEDSSSEDSADDSSSETKKKHKDEDWQMSGSGSVGTGS
DSESAEDGDKSSCEESEEDJ EPKNKVKSRKPPSRIKPKGKKSTGQKRRQLDSSE
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SVGYGSWBATKMDPDLSLTQKILPDDPDKRPGAKOLQOTRADYLIKLLKNLARKERAQ
RLAGAGNSKRKRYRKKNKKKKAKSK IKEEIKSDSSPQPSEKSDEDDEEEDVKDEIVSVK
HLHKKIRTEKENEEKPEPDIGIKKEAEEKRETKEKKENKRELKEEV
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ESEELHQKTFSVCKERMRPVKAALKQLDRPEKGLSEREQLEHTRQCLIKIGDHITECL
KEYTNPEQIKQMRKNLWIFVSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNVN
                                                                                                                                                                                                                        linked in the chicken Gallus domesticus
                                                                                                                                                                                                                                                                                          Griffiths, R. and Korn, R.M.
Direct Submission
Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 8Q0, UK
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SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"chromo-helicase-DNA-binding on the Z chromosome
                                                                    Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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/gene="CHD.2"
/function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in longer \
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1223 c 1520 g 1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAC60282.1"
/db_xref="GI:2501846"
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Griffiths, R. and Korn, R.M.
A CHD1 gene is z chromosome link
Gene 197 (1-2), 225-229 (1997)
97473516
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/gene="CHD-z"
     GI:2501845
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90.4%;
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                                                                       3303 GAAGATGATATTGAGTTGGAACCAGAAAGAAATTCAAGAAATTGGGAAGAAATCATCCCA 3362
                                                                                                                                              GGTTATGGCAGTTGGGAAATGATAAAAATGGATCCTGATCTCAGTTTGACACAGAAGATT 1140
                                                                                                                                                                                                                                               3543 CCAAAAAGGGGGGGAAGACCTCGAACCATTCCTCGAGAAAATATTAAAGGATTTAGTGAT 3602
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  0; Mismatches 125; Indels
Matches 1176; Conservative
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Medazoa, Chordata; Craniata, Vertebrata; Buteleostomi;
Bucharyota, Metazoa, Chordathae; Strigiformes; Strigidae; Aegolius.
1 (bases 1 to 2754)
Fridolfsson,A.K. and Ellegren,H. Molecular evolution of the avian CHDI genes on the 2 and W sex
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FridoLfsson.A.-K. and Ellegren.H.
FridoLfsson.A.-K. and Ellegren.H.
Submitssion
Submitted (30-AUG-1999) Department of Evolutionary Biology,
Evolutionary Biology Centre, Uppsala University, Norbyvagen 18D,
Uppsala S-75236, Sweden
                                                                1081 GGTTATGGCAGTTGGGAAATGATAAAAATGGATCCTGATCTCAGTTTGACACAGAAGATT 1140
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<1. .>2754
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Aegolius funereus chromosome W chromc
proctein 1 (CHDIW) mRNA, partial cds.
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AF181827 GI:5917751
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Wypphicus hollandicus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Psittaciformes; Cacatuldae;
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Fridolfsson, A.-K. and Ellegren, H.
Direct Submission
Submitted (30-AUG-1999) Department of Evolutionary Biology,
Evolutionary Biology Centre, Uppsala University, Norbyvagen 18D,
Uppsala S-75236, Sweden
2551 CCTTCAGATCCAGAAGACAGGAAAAGATATGTCATCCCATGCCACACCAAGGCAGCTCAT 2610
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/chronosome="W"
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Fridolfsson, A.K. and Ellegren, H.
Molecular evolution of the avian CHDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGATGGATATAGATGAAATCCTGAAGAGGNCTGAAACTCGAGAAAATGAGTCAGGCCCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360
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                                                                                                                                                                                                                                                                                                                                                                TTGAAGTTTGGTGCTGAGGAACTTTTTAAAGAACCTGAANNNGAAGAAGAGGAGCCTCAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          780
                                                                                                                                                                                                             61 AAGATGGTGTTAGATCATTTAGTGATTCAGAGAATGGACACCACAGGGAAAACTGTACTA 120
                                                                                             Gaps
                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1771 TIGAAGTITGGTGCTGAAGAACTITITAAAGAACCTGAAGGGGGAAGAAGAAGGAGGGCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2191 CCAAAAAACGFGGACGACCACGAACTATTCCTCGAGAAAAACATTAAAGGATTTAGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2251 GCAGAGATTAGGCGGTTTATCAAGAGTTACAAGAAATTTGGTGGCCCACTTGAAAGGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               841 AGAACAGGTGGTAGATTTGGGAAAGTTAAAGGCCCAACATTCCGAATAGCAGGAGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAAGAAA
                                                                                                                                                                                                                                                                                      CATACAGGCTCTACTCCTTCAAGCTCAACACCTTTTAATAAGGAAGAGTTATCAGCAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGATGACATTGAAATTGGAACCAGAACAAAATCTAAGAAACTGGGAAGAAATCATTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 GAAGTTCAGTGGCGACGAATAGAGGGGNNGGAAAGACAAAAAGAACTTGAAGAAATATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 ATGCTTCCAAGAATGAGAAACTGTGCAAAACAGATCAGCTTTAATGGAAATGAAGGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGAGATTAGACGATTTATCAAGAGTTACAAGAAATTTGGTGGCCCAGTTGAAAGGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGAACTTGTACATAATGGATGCATTAAGGCTTTAAATGATAATGACTTTGGTCAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAACTGTAGGAGATGAGTTACTTTCACAGTTCAAGGTAGCTAACTTTTCCAATATGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAAAAAACGTGGACGACCACGAACTATTCCCCGTGAAAACATTAAAGGATTTAGTGAT
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0
                                                       2754;
                                                                                             Indels
                                                       Length
                                                   Score 1054; DB 5;
Pred. No. 8.2e-227;
0; Mismatches 71;
                                                   Query Match 80.1%;
Best Local Similarity 93.9%;
Matches 1093; Conservative
                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                181
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Best Local Similarity
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                                                                                                                                                                                                          2071 ATGCTCCCAAGGATGAGAAACTGTGCAAAACAGATTAGCTTTAATGGAAGTGAAAGGAGA 2130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2311 GATGCTATAGCTAGAGATGCTGAGCTGGTTGATAAATCTGAGACGGACCTTAGACGTCTG 2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2371 GGAGAACTIGIACATAATGGATGCATTAAGGCTTTAAATGATAATGCTTTGTTCAAGAA 2430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTTCAGATCCAGAAGAAAGGAAAAGATATGTCATCCCATACCACACCAAAGCAGCTCAT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2551 CCTTCAGATCCAGAAGAAAGAAAAGATGTCATCCCATGCCACACTAAGGCAGCTCAT 2610
                                                                                                                                                                           61 AAGATGGTGTTAGATCATTTAGTGATTCAGAGAATGGACACCACAGGGAAAACTGTACTA 120
                                                                                                                                                                                                                                                                    121 CATACAGGCTCTACTCCTTCAAGCTCAACACCTTTTAATAAGGAAGATGTTCAGCAATT 180
                                                                                                                                                                                                                                                                                                                                                         181 ITGAAGTTTGGTGCTGAGGAACTTTTTAAAGAACCTGAANNNGAAGAAGAGGAGCCTCAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 GAGATGGATATAGATGCATGAAGAGGNCTGAAACTCGAGAAAATGAGTCAGGCCCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 TTAACTGTAGGAGATGAGTTACTTTCACAGTTCAAGGTAGCTAACTTTTCCAATATGGAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GAAGATGACATTGAATTGGAACCAGAACAAAATCTAAGAAACTGGGAAGAAATCATTCCA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 GAAGTTCAGTGGCGACGAATAGAGGGGNNGGAAAGACAAAAAGAACTTGAAGAAATATA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 ATGCTTCCAAGAATGAGAAACTGTGCAAAACAGATCAGCTTTAATGGAAATGAAGGGAGA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 CCAAAAAAACGTGGACGACCACGAACTATTCCCCGTGAAAACATTAAAGGATTTAGTGAT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 GCAGAGATTAGACGATTTATCAAGAGTTACAAGAAATTTGGTGGCCCAGTTGAAAGGTTA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           721 GATGCTATAGCTAGAGATGCTGAGCTAGTTGATAAATCTGAAACAGACCTTAGACGTCTG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   781 GGAGAACTTGTACATAATGGATGCATTAAGGCTTTAAATGATAATGACTTTGGTCAAGGA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         841 AGAACAGGTGGTAGATTTGGGAAAGTTAAAGGCCCAACATTCCGAATAGCAGGAGTGCAG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               901 GTGAATGCAAAGCTAGTCATTTCTCACGAAGAAGAGTTGGCACCATTGCATAAATCGATT 960
                                              0; Gaps
                                                                                     1 ATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAAGAAA 60
  DB 5; Length 2754;
                                              74; Indels
79.7%; Score 1049.2; DB 5, 93.6%; Pred. No. 9.8e-226; tive 0; Mismatches 74;
                    Best Local Similarity Matches 1090; Conservative
  Query Match
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QQ

QQ

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delta-crystallin enhancer binding protein, complete sequence.

D14316
D14316.1: G1:391639
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Submitted (29-JAN-1993) Jun-ichi Funahashi, Inst. Devel., Aging and
Cancer, Tohoku Univ.; 4-1 Seiryo-machi, Aoba-ku, Sendai 980-77,
Japan (Tel:022-272-9499, Fax:022-272-3982)
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BDDIELEPERNSRNWEELIPESGRERIEBERSOKELEETI-MLEMRACKAGISFNGSE
ERRERSRRYSGRSDSISTERKRYKRGRPTIPRENIKGFSDAEIRRFIKSYKRFGGF
LERLDAVARDAELVDKSETDLRRLGELVHNGCIKALKONSSGOBRAGGRLGKYKRFGF
RIGSVOVNAKLVISHEEELAPLHKSIPSDPERRKRYVIPCHTKAAHFDIDWGKEDDSN
LLGGIYEYAYGWGCKYNGSRSGLNTEILPDDPRTPRQNSYRPVQTTSLNY*

11 LJGIYEYAYGWGCKYNGSRSGLNTEILPDDPRTPRQNSYRPVQTTSLNY*

385 G 546 9
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VTKGSVEEDILERAKKKMYLDHLVIQRMDTTGKTVLHTGSTPSSSTPFNKEELSAILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MELKKCCNHCYLIKPPDDNEFYNKQEALQHLIRSSGKLILLDKL
LIRLRERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHPNAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="beta-gal fusion protein binds to blocks 10 to 3 of HN fragment of delta-crystallin enhancer."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                         1081 GGTTATGGCAGTTGGGAAATGATAAAAATGGATCCTGATCTCAGTTTTGACACAGAAGATT 1140
                                                                                                                                Gallus gallus (library: lambda gtll) 13 day embryo lens cDNA to
mRNA, clone JF11.
1021 TITGATATAGATIGGGGTAAAGAAGATGATTCCAATCTGTTAATAGGCATCTATGAATAT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Funahashi,J., Sekido,R., Murai,K., Kamachi,Y. and Kondoh,H. Delta-crystallin enhancer binding protein delta EF1 is a zinc finger-homeodomain protein implicated in postgastrulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opment 119 (2), 433-446 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="lens"
/clone_lib="lambda gtl1"
/dev_stage="13 day embryo"
257. 1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAA03262.1"
/db_xref="G1:391640"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1994)
Location/Qualifiers
1. .2292
                                                                                                                                                                                                                                           2731 TTACCTGATGATCAGATAAGAAA 2754
                                                                                                                                                                                                               1141 TTACCTGATGATCCAGATAAGAAA 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 2292)
Funahashi,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 2292)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
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Score 1030.4; DB 5; Length 2292; Pred. No. 1.7e-221;

78.38;

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/product="chromodomain helicase DNA binding protein 1"
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/protein_id="AAD56022.1"
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WEDGALIAKKFQTCIDEYFSRQSKTTPFKDCKVLKQRPRFVALKKQPSYIGGHEGLE
LRDYQLNGLMWLAHGSWCRGSIAADEMGLKATIOTFSLAYLFHEHGLYGPFLLVVP
LSTLISWORELGTWAPQMNAVVYLGDITSRNMIRTHEWHLLITGTPLQNSFLLVVP
LSTLISPIMPERFSSREDFEBEHGKGREYGYASLHKELEPFLLRRYKRDVEKSLPAKVED
ILRMEMSALQKQYYKWILTRNYKALSKGSKGSTGFLNIMMELKKCCNHCYLIKPPDG
NEFYNKQBALQHLIRSSGKLILLDKLLIRLERGRRVLIFSQWYRLDILARYLKYQ
ILRMEMSALQKQYYKWILTRNYKALSKGSKGSTGFLNIMMELKCCNHCYLIRPDG
NEFYNKQBALQHLIRSSGKLILLDKLLIRLERGRRVLIFSQWYRLDILARYLKYQ
NEFYNKQBALQHLIRSSGKLILLDKLLIRLERGRRVLIFSQWYRLDHLYQRNDTTG
KYVLHTGSTPSSSTPFNKEELSAILKFGAEELFKEPEGEGEBQEDQHDIDEILKRAETR
RUPQRLGAGARARRACKQVNIYRLYKGAEELFKEPEGEGEBQEPQEMDIDEILKRAETR
RUPGPLTVGDELLSQFKVANFSNNDEDDIELEPENNSRNWEEIIPEVQRRRIEBEER
QKELEEIYMLPRARNCAKQISKGGFLERLDAAARDAELVDKSSTDLRRLGELVHNGC
IKALKDSSSGGERAGGRLGSKYKGFPFRISGYQVNAALVISBEEELAPLHKSIPEDD
NOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p mRNA linear VRT 07-AUG-2001
chromodomain helicase DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Strigiformes; Strigidae; Aegolius. [ thases I to 2754)
Fridolfsson, A. K. and Ellegren, H. Molecular evolution of the avian CHDI genes on the Z and W sex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eridolfsson, A.-K. and Ellegren, H.
Direct Submission
Submitted (30-AUG-1999) Department of Evolutionary Biology,
Evolutionary Biology Centre, Uppsala University, Norbyvagen 18D,
Uppsala S-75236, Sweden
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Direct Submission
Submitted (30-AUG-1999) Department of Evolutionary Biology,
Evolutionary Biology Centre, Uppsala University, Norbyvagen 18D,
Uppsala S-75236. Sweden
Location/Qualifiers
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                                                                                                       1021 TTTGATATAGATTGGGGTAAAGAAGATGATTCCAATCTGTTAATAGGCATCTATGAATAT 1080
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/strain="Lutino cockatiel"
/db_xref="taxon:13180"
/chromosome="2"
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KGSVEEDILERAKKRVLDHJUDRWDTTGKTVLHTGSAPSSTPFRKEELSAILKFG
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Woodage,T., Basrai,M.A., Baxevanis,A.D., Hieter,P. and Collins,F.S. Characterization of the CHD family of proteins
Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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Catarrhini; Hominidae; Homo.
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Submitted (03-JUN-1997) Laboratory of Gene Transfer, National is Genome Research Institute, National Institutes of Health, 49 Convent Drive, Bethesda, MD 20892-4442, USA Location/Qualifiers
TTTGATATAGATTGGGGTAAAGAAGATGATTCCAATCTGTTAATAGGCATCTAATAT
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/db_xref="G1:2645429"
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/db_xref="taxon:9606"
/chromosome="5"
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Mammalia; Eutheria; Primates;
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1. .5947
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164. .5293
/gene="CHD1"
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Woodage,T.
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EALSGAGSSKRRARARKNKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLSESKSDGR
ERSKKSVBAPUHITAGSGEPVETSESEELDOFUTFEICKERNRPVKAALKQLDRPEK
GLSEREQLEHTRQCLIKIGDHITECLKEYTPPDEJKOMRKNLMIFVSKFTEFDRRLH
KLYKHAIKKESEQQASDQNSDQNSNLMPHYTRNPDVERLKEWTNHDDSSRDSYSSDRHLTQ
YHDHKDRHQCDSYKKSDSRKRPYSSFSNGKDHRWDHYKQDSRYYSDRHLTDH
RSRDHKSNLEGSLKDRSHSDHRRASSDHRLHSDHRSSSEYTHHKSSRDYRYHSDWDMDH
RASSSGRRSPLDQRSYGSRSPFBHSYDHKKSTPEHTWSSRYT"

1004 c 1243 g 1570 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGTICAGTGGCGACGAATAGAGGGGNNGGAAAGACAAAAAGAACTTGAAGAATATAT 480
                                                                                                                                                                                                                                                                                          AAGATGGTGTTAGATCATTTAGTGATTCAGAGAATGGACACCACAGGGAAAACTGTACTA 120
                                                                                                                                                                                                                                                                                                                                                    CATACAGGCTCTACTCCTTCAAGCTCAACACCTTTTAATAAGGAAGAGTTATCAGCAATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTAACTGTAGGAGATGAGTTACTTTCACAGTTCAAGGTAGCTAACTTTTCCAATATGGAT 360
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                                                                                                                                                                    Score 959.6; DB 9; Length 5947;
Pred. No. 1.3e-205;
0; Mismatches 210; Indels 6;
                                                                                                                                                                  Query Match 72.9%;
Best Local Similarity 83.6%;
Matches 1098; Conservative (
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                                                                                                         BASE COUNT
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Mammalia: Eutherla: Rodentla: Sciurognathi; Muridae; Murinae; Mus.

1 (Dasses 1 to 5349)

Delmas, V., S.Cokes, D.G. and Perry, R.P.

A mammalian DNA-binding protein that contains a chromodomain and an SNF2/SWIZ-like helicase domain

Proc. Nall. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
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RKQPQQAQQQRPASSNSGSEDDSDSSGAKRKKHNDEDWOMSGSSPSQLG
SDSESEERDKSSCOTESDY PRKVVRSRKPQNRSKSKNGKTLLGQKKRQIDSSEDD
DDEDYDDNRSSRQATVWYSYKEDEBWKTDSDDLLEVCGEDVPOPEDEFFFT IRRW
DCENVGRKGATGATTTIYAVBADGDPNAGFERNKEPGDIQYLIKWKGWSHIHNTWETEE
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Direct Submission
Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA
On Feb 16, 1994 this sequence Version replaced 91:293322.
                                                                                      1020
                                                                                                                                              CTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAGAGACTTGCTGGTGCA 1260
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                                                                                      CCTTCAGATCCAGAAGGAAAGGATATGTCATCCCATACCACCAAAGCAGCTCAT
                             GTGAATGCAAAGCTAGTCATTTCTCACGAAGAGAGTTGGCACCATTGCATAAATCGATT
                                             1261 GGCAATTCAAAGAGGAGAAAAACAAGAAGTAAGAAGAATAAAGCAACAAGGCT 1314
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/protein_id="AAB08486.1"
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/organism="Mus musculus"
/db_xref="taxon:10090"
/cell_type="plasmacytoma"
1. .5349
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171. 5306
/gene="CHD-1"
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TLKQONVRGMKKLDNYKKKDQETKRWLKNASPEDVBYYNCQQELTDDLHKQYQIVERI
TAHSNQKSAAGLDNYCKKOGLPYSECSWEDGALISKKFQYCIDEYFSRNQSKTTPFK
DCKVLKQRPRFVALKKQPSYIGGHEGLELKYPYGLNGLNWLAHSWCKONSCILADEMGE
GKTYLKQRYFFFFYALKYGPSYIGGHEGLELKYPYGLNGLNWLAHSWCKONSCILADEMGE
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YKTLLIDFKSHNRLLITGTPLONSKELMPAYDOILGHENGESSWGDFEEBEHGKGRENGYR
SLHKELEPPLLRYKKKDVBKSLPARVEOILGHENDENSALOKOYYKWILTRNYKLLSKG
SLEKEREPPLRRYKKLDYRSCLPARVEOILGHENGSALOKOYYKWILTRNYKLLSKG
STSGFLNIMMELKKCCNHCYLIKPPONNEFYNKQBALQHLIRSGKLJLIRL
RERGNYRVLLISGANVANLDILLASLYKKRGFPPQLAGSTRGELKGAADHFNABGSEDF
CFLLSTRAGGLGINLASADTOWILFDSDWNPONDLQAQARAHRIGQKKQVNIYRLYKG
SVEEDILERAKKKWVLDHLVIQRMDTGKTVLHTGSAPSSSTPFNKEELSAILKFGAE
ELKREBEGEREDEPORDOIDETLKRAETHENEPCPLLSVGDELLSGFKVANFSNNDEDDI
ELEPERNSKNWEETIPERGYRKRGRPRTIPRENIKGFSOBELSGKVANFSNNDEDDI
ELEPERNSKNWEETIPERGYRKLEETINGSSSGTERAGKKVKGFRSA
NOVNAAKLYTHABDELIPLHKSIPSRCKALKSSSGTERAGKKVKGFRSA
ORLCGAGGSKRRWRAKSKRKRKTKTRENIKGESTSTSTRETKSYKKFGBDLLIG
INEYGYGSRRRYRRAKKSKRAMKSIKVREETKSDSSGTERAGKLYKOTTRILLSRDIAKREA
GLSKRSQLEHTRQCLIKTILDDPDKKRQARQLQTRADYLIKLLSRDIAKREA
GLSKRSQLEHTRQCLIKTILDDPDKKRYGNENIKTSCSCTEREMRPVKAALKCLDRPEK
GLSRRSQLEHTRQCLIKTATHYGUKEYSNPDQTIKWRNNINTFVSKFTEFDRAKKLH
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HRSREHRPSLEGGLKDRCHSDHRSHSDHRMHSDHRSSSEHTHHKSSRDYRYLSDWQLD
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79.4%; Pred. No. 9.1e-189;
ive 0; Mismatches 270; Indels 0;
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CCAAAAAAACGTGGACGACCACGAACTATTCCCCGTGAAAACATTAAAGGATTTAGTGAT

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Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae;
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GGTTATGGCAGTTGGGAAATGATAAAATGGATCCTGATCTCAGTTTGACACAGAAGATT 1140
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Submitted (21-APR-1997) A.K. Fridolfsson, Swedish Univ. of
Agricultural Sciences, Animal Breeding and Genetics, Box 597,
24, Uppsala, SWEDEN
                                                  TTACCTGATGATCCAGATAAGAAACCCCAGGCTAAGCAGTTACAGACTCGTGCAGATTAC
                                                                                     GATGCTATAGCTAGAGATGCTGAGCTAGTTGATAAATCTGAAACAGACCTTAGACGTCTG
                                                                                                   GGAGAACTTGTACATAATGGATGCATTAAGGCTTTAAATGATAATGACTTTGGTCAAGGA
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                                                                                                                                                                                                      CGAGCAGGTGGCAGATTGGAAAAGTGAAGGGCCAACATTCCGCATCTCTGGAGTCCAA
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Ficedula albicollis.
Ficedula albicollis.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
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Male-driven evolution of DNA sequences
Nat. Genet. 17 (2), 182-184 (1997)
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Fridolfsson, A.K.
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Submitted (21-APR-1997) A.K. Fridolfsson, Swedish Univ. of Agricultural Sciences, Animal Breeding and Genetics, Box 597, S-75124, Uppsala, SWEDEN
             VRT 07-FEB-2002
                                                            CHDIW gene; chromodomain-helicase-DNA-binding protein.
yellowhammer.
Emberiza citrinella
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
Fringillidae; Emberizinae; Emberiza.
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                linear
                                                                                                                                               1 (sites)
Ellegren, H. and Fridolfsson, A.K.
Male-driven evolution of DNA sequences in birds
Nat. Genet. 17 (2), 182-184 (1937)
                                                                                                                                                                                                                                                                                 Location/Gualifiers
1. 615
7. organism="Emberiza citrinella"
/db_xref="taxon:37595"
/chromosome="W"
/tissue_type="blood"
/dv_stage="adult"
1. 615
                DNA
             ECY12940 615 bp DN;
Emberiza citrinella CHDIW gene, exon.
                                                                                                                                                                                                                                                                                                                                                                                       /gene="CHD1W"
1..615
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<1. .>615
                                                   Y12940.1 GI:2765287
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Fridolfsson, A.K.
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Submitted (21-APR-
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                         DEFINITION
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                                                                                                                                                                                                                                                                                                  41.8%; Score 549.8; DB 5; Length 615; 93.0%; Pred. No. 2.1e-113; tive 0; Mismatches 43; Indels 0.
/organism="Ficedula albicollis"
/db_xref="taxon:59894"
/chromosome="W"
                                      /tissue_type="blood"
/dev_stage="adult"
1 .615
/gene="CHDIW"
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<1. .>615
                                                                                                                               /gene="CHD1W"
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nes 572;
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Best Local S:
Matches 572,
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Eridolfsson, A.K.
Direct Submission
Submitted (21-APR-1997) A.K. Fridolfsson, Swedish Univ. of
Agricultural Sciences, Animal Breeding and Genetics, Box 597, S-751
24, Uppsala, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yellowhammer.
Emberiza citrinella
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
Fringillidae; Emberizinae; Emberiza.
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                                                                                                                         61 AGAATGGACACTACAGGGAAAACTGTGTTACATACAGGCTCTACTCCTTCAAGCTCAAAC 120
                                    241 GCTGAAACTCGGGAAAATGAGCCAGGTCCATTAACTGTAGGAGATGAGTTGCTTTCGCAG
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Ellegren, H. and Fridolfsson, A.K.
Male-driven evolution of DNA sequences in birds
Nat. Genet. 17 (2), 182-184 (1997)

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   Matches 558;
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EELGAILKEGAEELEKEPEGEEQEPQEMDIDEILKRAETRENEPGPLTVGDELLSQFK
VANFSNMDEDDIELEPERTSKNSNWEEIIPEVQRRRIEEEERQKELEEIYMLPRMRNCAK
QISPNGSEGRRSRSRSKSSDSJESERKRFKKRGRPRTIPRENI"
95 c 159 9 131 t
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Submitted (21-APR-1997) A.K. Fridolfsson, Swedish Univ. of
Agricultural Sciences, Animal Breeding and Genetics, Box 597, S-751
24, Uppsala, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae;
Ficedula.
                                                                                                                         570
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                                    391 AATCTAAGAAACTGGGAAGAAATCATTCCAGAAGTTCAGTGGCGACGAATAGAGGGGGNNG
                                                                                                                                                                                                                                                 571 GATAGTGATTCCATCTCAGAAAGAAACGACCAAAAAAACGTGGACGACCACGAACTATT
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Ficedula albicollis.
Ficedula albicollis
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Ellegren, H. and Fridolfsson, A.K.
Male-driven evolution of DNA sequences in birds
Nat. Genet. 17 (2), 182-184 (1997)
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Pred. No. 2.2e-108;
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1. .613.
/organism="Ficedula albicollis"
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/tissue_type="blood"
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1. 615
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/gene="CHD1Z"
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Job time: 26872 sec

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GISFNGSEGRRSRSRRYGGSDSOSISBRKRFKKRGRPRTIPRENI"
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<1. .>615
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                                                                                      61 CAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTT 120
                                                                                                         CAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTT 120
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Pred. No. 7.4e-32;
0; Mismatches 8;
                  Score 153; DB 6;
Pred. No. 1e-35;
; Mismatches 0;
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                                                                                                                                                                Patent: WO 9639505-A 3 12-DEC-1996,
ISIS INNOVATION (©B)
Other publication AU 5906996 961224
Location/Qualifiers
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Sequence 3 from Patent W09639505.
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1 (bases 1 to 153)
Griffiths, R. and Tiwari, B.
                  Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 153; Conservative 0;
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94.8%;
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
BIRDS
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS
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Pred. No. 6.3e-30;
0; Mismatches 12;
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Pred. No. 2.1e-21;
0; Mismatches 29;
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                                   Patent: WO 9639505-A 5 12-DEC-1996,
ISIS INNOVATION (0B)
Other publication AU 5906996 961224
Location/Qualifiers
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34 c 31 g 28
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Other publication AU 5906996 961224.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 bp
Sequence 2 from Patent WO9639505.
A58683.
A58683.1 GI:3714246
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                                                                                                                                                                                                                                                Query Match 87.5%;
Best Local Similarity 92.2%;
Matches 141; Conservative
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Best Local Similarity 80.9%;
Matches 123; Conservative
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DDBEDTURKGSRRQATUNGY KERETYTDSDDLLEVGEBUYPQTEEDEFFILEKFND
SRIGRKGATAGATTIAVENDEDANGTEERSKELEGETGUTGUKKGWSHIHWWETEET
LKQONYKGMRKLDAYKKDDETKRWLKNASPEDDEY YNCOELTDDLHKYWETEET
LKQONYKGMRKLDAYKKDDETKRWLKNASPEDDEY YNCOELTDDLHKYWETEET
LKCONYKGMRKLDAYKKDDETKRWLKNASPEDDEY YN OCOELTDDLHKYWETEET
AHSNOKSAAGYPDYYCKWOGLPYSECSWEDGALIAKKFQARIDEYFSRNOSKTTPFKD
CKYLKORPRYALKKOPSTGGARSLEEDROYOLGHWALHSWKGWSHITPPKD
CKYLKORPRYALKKOPSTGGARSLEEDROYOLGHWALHSWARGNGTADENGKGREI
KTIGTISCHANTLEHBOLYGPFLLKPULSTTGGBRELERROYKGNSCILTAROYKERSHILKNADDSLLY
RTLIDFRENSHHLLITGTPLONGSLEELMSLHFINPERFSGMEDFEEGRGREYGYSS
LHKRLEPFLLRRVKROVEKSLPANVOOTILRMENSALOKOYYKWILTRNYKALGKGSKG
STGFLAHMWELKKCNHOYTIKPOPSTGLANGSALOKOYYKWILTRNYKALGKGSKG
FLLSTRAGGLGINLASADTVVIFDSDWNPQNDLOAQARAHRIGGKKOVNIYRLVTKGS
VERDILERRYKKKWULDHLYGYRWYRGPFORLDGSIKGEERRYAALGHGKKKWYNIYRLVTKGS
VERDILGERRYKKKWULDHLYGYRWYRGPFORLDGSIKGSTSSSTPREELSALIKFGARE
LKREPGEGOGPOODNIDELLKRAFTRENBEGFLYVGDELLSOFWANTSNUDEDIE
                                                                                                                                                                                                                                                                                                                                           Gallus gallus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 6872)
Griffiths, R. and Korn, R.M.
A CHD1 gene is Z chromosome linked in the chicken Gallus domesticus
Gene 197 (1-2), 225-229 (1997)
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AVARDAELVDKSETDLRKLGELVHNGCIRALKDNSSGOBRAGGRLGKWGPTFRISGY
QVNARLY UISHEEELAPLHKSIPSDPEERKRY VIPCHTRAAHFDIDMGKEDDSNLLVGI
YEYGYGSWEMIKTMEDPLSLTQKILLPDDPDFKPQAKQLOTRAANII KLLINKDLARKRAO
RLAGAGNSKRRKTRNKKNKMKASKIKEEIKSDSSPQPSEKSDEDDEEEDNKDEIVSYK
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ESEELHOKTFSVCKERMRPVKAALKOLDRPEKGLSEREQLEHTROCLIKIGDHITECL
KEYTNPEQIKOWRKNLMIEVSKFTEFDARKLHKLYKHAIKKROGSQOHNDONISSNVN
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SAFSKCHRROMDHYKOOSYYSOSKIRKLDBOHRSROHSSULEGULKOSRGHSBHRSH
SOHRIHSDKHROMDHYSEYSHKSSRDYRYHBOWQMDHRASGSGFRSPLORSFSPLO
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Ab_xref="G1".201846"

Aranslation="MNGHSDEBSYRNSGGESSRSDDDSGSASGGSGSSSGGSSBGGSS

SOGGSGSDSEGSCSGSESESTTSRKRQVARPRAGOSSEFWRSSPILAVORSAG

SOGGSSDSEGSGSSGSESESTTSRKRQVARPRAGOSSEFWRSSPILAVORSAG

LKKQOQOQKAASSDGSESESDSSSEEDESDSSSEEDESDSSSEEDES

DSSSASDGGSESSSDSSSEEDESSSEEDESSEEDES

DSSSASDGGSESSSDYEPRINKVKSRKPPSRIKPKSGKRSTGQKKRQLDSSEEEE
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     VRT 08-OCT-1997
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Griffiths,R. and Korn,R.M.
Direct Submission
Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University,
Glasgow G12 800, May
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AF004397 G872 bp mRNA linear VRT 08-OCT-19
Gallus gallus chromo-helicase-DNA-binding on the Z chromosome
protein, varian thth hydrophilic domain, (CHD-2) mRNA, complete
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/function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
/codon_start=1
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/db_xref="taxon:9031"
1. 6872
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228. .5654
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                                                /your short insert found in longer variant mRNA of CHD-Z"/note="short insert found in longer variant mRNA of CHD-Z" 1223 c 1520 g 1683 t
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/clone_lib="lambda gt11"
/dev_stage="13 day embryo"
257. 1939
/note="beta-gal fusion protein binds to blocks 10 to 3 of HN fragment of delta-crystallin enhancer."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 2292)
                                                                                                                                                                                                                                                                                                                                                                            51 CAAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAA 110
                                                                                                                                                                                                                                                                              Gaps
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Delta-crystallin enhancer binding protein delta EF1 is a zinc
finger-homeodomain protein implicated in postgastrulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D14316 2292 bp mRNA linear VRT 03-FE
delta-crystallin enhancer binding protein, complete sequence.
D14316
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                                                                                                                                                                                                              Length 6872;
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                                                                                                                                                                                                           Score 95; DB 5; Le
Pred. No. 2.4e-18;
0; Mismatches 5;
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/organism="Gallus gallus"
/db_xref="taxon:9031"
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/db_xref="GI:391640"
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4341. .4604
/gene="CHD-2"
                                                                                                                                                                                                              62.1%;
ilarity 95.1%;
Conservative
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Funahashi,J.
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CFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGGKKQVNIYRLVTKG
SVEEDILERAKKKMVLDHLVIQRMDTTGKTVLHTGSAPSSSTPFNKEELSAILKFGAE
ELFKEPEGEEGEPOPMOIDELIKRAETHBNEPQELSVGDELLSQFKVANFSNNDEDDI
ELEPERNSKNWEEII PEEGREKLEEEROKELEEIYMLPRAKNCAKOISFNGSGRRS
RSRRYSGSDSDSISERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLERL
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DDEDYDNDKRSSRRQATVNVSYKEDEEMKTDSDDLLEVCGEDVPQPEDEEFETIERVM
DCRVGRKGATGATTIIYAVEADGDPNAGFERNKEPGDIQYLIKWKGWSHIHNTWETEE
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IAHSNOKSAAGLPDYYCKWQGLPYSECSWEDGALISKKFQTCIDEYFSRNQSKTTPFK
DCKVLKQRPRFVALKKQPSYIGGHEGLELRDYQLNGLNWLAHSWCKGNSCILADEMGL
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NMIRTHEWHHPOTKRLKFNILLTTYEBILLKDRAFLGGLNWAFIGVDEAHRLKNDDSLL
YKTLIDFKSNHRLLIGTPLONSLKELWSLLHFINPEKFSSWEDFEEBHGGREYGYA
SLHKELBEPFLLRRYKRUYEKSLPARVBOILEMMMSALOKQYYKWILTRNYKALSKGSK
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RKQPQQAQQQRPASSNSGSEEDSSSSEDSDDSSSGAKRKKHNDEDWQMSGSGSPSQLG
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RERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHFNAEGSEDF
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Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center,
7701 Burholme Avenue, Philadelphia, PA 1911, USA
On Feb 16, 1994 this sequence version replaced gi:293322.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi: Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 5349)
Delmas, V., Stokes, D.G. and Perry, R.P.
A mammalian DNA-binding protein that contains a chromodomain and a SNF2/SWI2-like helicase domain
                                                                                                                                                                                                                                                                     53 AGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAATA 112
                                                                                                                                                                               Gaps
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2 (bases 1 to 5349)
                                                                                                              Length 2292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          אסט השוון mRNA linear F 5349 bp mRNA linear F Mouse DNA-binding protein (CHD-1) mRNA, complete cds.
LIOLIO X66028
                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                      113 AAGACCTTGCAAGAAAGGAAG--CACAGAGACTTGCTGGTGCA 153
                                                                                                           Score 69.8; DB 5;
Pred. No. 1.1e-10;
0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="DNA-binding protein"
/protein_id="AAB08486.1"
/db_xref="GI:455015"
   534
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/db_xref="taxon:10090"
/cell_type="plasmacytoma"
1. 5349
546 g
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171. 5306
/gene="CHD-1"
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                                                                                                              45.6%;
ilarity 86.4%;
Conservative
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385
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                                                                                                                                             Best Local Similarity
Matches 89; Conserv
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The same of

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DAIARDAELVDKSETDLRRLGELVHNGCVKALKDSSGTERAGGRLGKVKGPTFRISG
VQVANKLVTAHEDELTELHKSIPSEDPERKGYGTTEOHTRAAHDIDMSKEDDSKLLIG
TYEVGYGSWARLTKAHPEDLEATHELSPEDFERKOTTEOHTRAAHDIDMSKEDDSKLLIG
TYEVGYGSGSRRKTTAKSKAKAKSKAKSTSOSPLESEKSDEDDDSKLUNSKEPESK
ORLCGAGGSKRRYTAKKSKAKAKSIVKEETTSOSPLESEKSDEDDDSKLUNSKEPESK
DENSKKSVVSDAPVHTTASGEPVITAESEELDGKTFSICKERNRIDDSSKSDYSSDSPS
GLSEREQLEHTRQCLIKIGDHITECLKEYSNPEDIKKNIMIFVSKFTEFDARKLI
KLYKRIAIKKNGESQONDONSNANYATHVITANDEMEKRYDDSKSYSDSYSSDRIS
OYHDHHKDRHQCOSYKKKSDSRRRPYSFSKOKCHREWDHYRGOSSYKSPRENKLID
HRSRERPESLEGGLORGISSHRPYSFSFOKOKHREWDHYRGOSPKYSDREKHKLDD
HRSRERPESLEGGLORGISSHRPYSFSFOKOKHREWDHYRGOSPKYSDREKHKLDD
HRSRERPESLEGGLORGISSHRPYSFSHOKHRIDHSSRRIT"

1067 C 1319 9 11224 L
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EETLKQQNWRGMKKLDNYKKKDOETKRMIKNASPEDVETYNCQOELTDDLHKQYQIVG
RIIAHNGKSAAGYPYCKWGQETPSECSWEDGALISKKPQACIDETFSRNGSKTTP
FKDCKVLKQDREFVALKROPSITGGHEGLEKBYQLNGINWIAHSWCKGNSCITADEM
GLGKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSWQREIQTWASQMNAVVYLGDIN
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1. (bases 1 to 5947).
Woodage,T., Basrai,M.A., Baxevanis,A.D., Hieter,P. and Collins,F.S. Characterization of the CHD family of proteins
Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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DDDEEDYDNDKRSSRRQATVNVSYKEDEEMKTDSDDLLEVCGEDVPQPEEEEFFTIER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                             ch 15milarity 45.1%; Score 69; DB 10; Length 5349; B 10.2%; Pred. No. 1.7e-10; 81; Conservative 0; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="5q15-21; near WI-5811"
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/db_xref="G1:2645429"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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164. .5293
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/gene="CHD1"
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Best Local Similarity
Matches 81; Conserva
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REFERENCE
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TITLE
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TITLE
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SRNMIRTHEWTHHOTKRIKFNILLITTELLKDKAFLGGLWAPIGUDEAHRLKNDDS
LLYKTLLDREKSBAFLLITGTPLONGLKERWELLHFTPREKSSREDFEREBRGKGREY
VASCHSGEVEN HUNDELKKCOHCYLIKPONDLENDREYSALDREEBERGKGREY
KASCHSGEVIN HUNDELKKCOHCYLIKPONDLENDREYKROEALOHITRSGKLILLDKLIL
RLABRAGKHYLIFSGKLILLDKLIL
RLABRAGKHYLIFSGKLILLDKLIL
RLABRAGKHYLIFSGKLUTTENSCHLILLDKLIL
RLABRAGKHYLIFSGKLUTHUNGLANDTONDLOAORAHRIGOKKOVNIYRLY
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AEEL-REPERGERGEPEDENDLEILYARAFTHENBEGFLTVODELLAGFKVANFSNNOBD
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IGTYBOYGSSWERMIRMODILSLTHKILPDDDPOKREDGAROLGTRANDYLIKILLSBULAK
EALSGAGSSPERRARAKKNRAMKSINVEETKSDSSCFERSCKSCR
ERSKRRARAAKKNRAMKSINVEETKSDSSCFERDOMLLSSEKSCGR
ERSKRRARAAKKNRAMKSINVEETKSDSSCFERDDDOMLESSEKSCGR
ERSKREKARAAKKNRAMKSINVEETKSDSSCFERDOMLAKESSKESCR
ERSKRSOYSDAPVHITAGGEDYTTECLKEYTHPEQLIKQHRONLMIFYSKFTEFDARKLH
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YHDHRORHQCDSYKKSDSRREPSSFSNGKDHROWDHYKQDSRYYSDREKHRKLDDH
RSRDHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSSEYTHHKSSRDYRYHSDWDH
RASSSGRREPLDORSYGSRSPFEHSVBHKSTPEHTWSSRRY"
1004 C 1243 g 1570 t
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Finishing Completed at Stanford Human Genome Center
Finishing Completed at Stanford Human Genome Center
Quality: Phrap Quality >-40 100% of Sequence;
Estimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624.
The number of bases overlapped is 90404.
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Submitted (03-JuL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (Dases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94589, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
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1 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence
AC092372
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DOE Joint Genome Institute.
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FEATURES

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Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 118268 AAAAAAACCACAAACAAAACAGTTGCAGACCCGTGCAGACTACCTCCATCAAATTACTTAGT 118327
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                     Homo sapiens chromosome 5 clone CTD-2082117, complete sequence. AC012624.6 GI:14993679
                                                                                                                                                                                                                                52 AAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
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DOE Joint Genome Institute and Stanford Human Genome Center
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Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                          Length 101220;
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                                                                                                                                                          Score 61; DB 9;
Pred. No. 3.6e-08;
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                                                                  /clone="RP11-58M12"
18862 c 17827 g 30409
1. .101220
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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DOE Joint Genome Institute.
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Dipublished

Sharea, N. Bedar, E., Abraham, H., Allen, N.,

Bairen, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Boduslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

DeArellano, K., Dewar, K., Domino, M., Doyle, M., Calagan, J.,

Ferrelra, P., FitzHugh, M., Forrest, C., Gage, D., Galagan, J.,

Fardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,

Macdonald, P., Marquis, N., Mebans, C., Mourk, A., McKernan, K.,

Macdonald, P., Marquis, N., Mebans, L., Morrow, J., Naylor, J.,

Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K.,

Plerre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,

Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,

Zimmer, A. and Zody, M.,

Direct Submission

Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 0211, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                   ACO21449 143079 bp DNA linear HTG 10-SEP-2000
Homo sapiens clone RP11-58M12, WORKING DRAFT SEQUENCE, 10 unordered
pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 143079)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
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Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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Center clone name: 58_M_12

Center clone name: 58_M_12

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 137473 bases at least Q40

Consensus quality: 140814 bases at least Q30

Consensus quality: 140814 bases at least Q20

Insert size: 144000; agarose-fp

Insert size: 142179; sum-of-contigs
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Contact: sequence_submissions@genome.wi.mit.edu
Db 118328 AGAGATCTTGCAAAAAAAAGAAGCTC 118352
                                                                                                                                                                                                                                                                             AC021449
AC021449.3 GI:10047806
HTG; HTGS_PHASE1; HTGS_DRAFT
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38820: contig of 38820 bp in length

34.

Mon Aug

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Consensus quality: 139128 bases at least Q40
Consensus quality: 14754 bases at least Q30
Consensus quality: 14754 bases at least Q30
Consensus quality: 14374 bases at least Q30
Estimated insert size: 145005; sum-of-contigs estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a "working draft' sequence. It currently

* consists of 7 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-M09-1999) Production Sequencing Facility, DOE Joint Submitted (03-M09-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced gi:7528342.
                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145659)
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* provided by the Submitted:

* by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 56174: contig of 56174 bp in length 56175 56774: gap of unknown length 100875 100974: gap of unknown length 100875 113127: contig of 1213 bp in length 113128 113127: contig of 1213 bp in length 113128 118190: contig of 14963 bp in length 118191 118694: contig of 14963 bp in length 11827: gap of unknown length 11827: contig of the print length 11827: contig of 1404 bp in length 118291 118694: contig of 1404 bp in length 119595 123297: contig of 303 bp in length 119595 123397: contig of 303 bp in length 123398 123397: contig of 22262 bp in length 123398 145559: contig of 22262 bp in length
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Center clone name: CIT-HSPC_480B11
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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Unpublished
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DOE Joint Genome Institute.
                                                                                                                                                               1 (bases 1 to 145659)
DOE Joint Genome Institute.
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                                                         Homo sapiens
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38821 38920: gap of 100 bp 4011: contig of 1191 bp in length 40412 40111: gap of 100 bp 40512 43179: contig of 2768 bp in length 40512 43180 4339; gap of 100 bp 43380 45906: contig of 2768 bp in length 43380 4005: gap of 100 bp 43380 47006 51830: contig of 4825 bp in length 51831 51930: gap of 100 bp 51931 62619: contig of 10689 bp in length 6262 62719: gap of 100 bp 62720 75408: contig of 12689 bp in length 75409 75809: gap of 100 bp 75809 92516: contig of 17008 bp in length 75409 75809: gap of 100 bp 75809 92516: contig of 13793 bp in length 106410 106599: gap of 100 bp 100 bp 106410 106499: contig of 36570 bp in length 106410 106599: gap of 100 bp 100 bp 
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Consensus quality: 180259 bases at least Q30
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Consensus quality: 184175 bases at least Q30
Consensus quality: 184175 bases at least Q30
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                         AC091946 193446 bp DNA linear HTG 09-JUN-2001 Homo sapiens chromosome 5 clone RP11-36012, *** SEQUENCING IN PROCRESS ***, 33 unordered pieces.
                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequencing of Human Chromosome 5
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Center clone name: RPCI-11_36012
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2: gap of unknown length
3: gap of unknown length
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1: contig of 9180 bp in length
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2: contig of 930 bp in length
3: gap of unknown length
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35252 c 37061 g 60360 t 3202 others
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82.4%; Pred. No. 3.4e-08;
ive 0; Mismatches 15; Indels
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A58686 Sequence 5
A58885 Sequence 4
A58681 Sequence 3
A58681 Sequence 3
A58681 Sequence 10
A58691 Sequence 10
A58691 Sequence 10
A58691 Sequence 15
L10410 Mouse DNA-D
D14316 delta-cryst
AC021224 Homo sapi
AC02124 Homo sapi
AC02124 Homo sapi
AC02124 Homo sapi
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AC03131 Homo sapi
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AC0314 Homo sapi
AC03185 Drosophil
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AC013881 Drosophil
AC003187 Homo sapi
AC003181 Homo sapi
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AC01381 Homo sapi
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Griffiths, R. and Tiwari, B.
AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224
Location/Qualifiers
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/organism="unidentified"
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Sequence 5 from Patent WO9639505.
A58686 1 GI:3714249
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2 AC016087
9 AC090819
6 AX333515
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2 AC074383
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10 AC013394
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153
1 ATTITACCTGATGACCCAGA.....TGCAAAGACTTACTGGTGCA 153
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                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                      61 CAGGCAAAGCAGTIGCAGACCCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTT 120
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Pred. No. 4.7e-29;
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                       100.0%; Score 153; DB 6; 100.0%; Pred. No. 1.1e-34;
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Griffiths, R. and Tiwari, B.
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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Pred. No. 4.2e-28;
0; Mismatches 14;
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Pred. No. 9.5e-21;
0; Mismatches 29;
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                                Patent: WO 9639505-A 3 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224
Location/Qualifiers
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Best Local Similarity 90.8%;
Matches 139; Conservative
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Best Local Similarity 80.9%;
Matches 123; Conservative
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AUTHORS TITLE

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FEATURES

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KEYWORDS

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SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
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4341. 4604
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1 1223 c 1520 g 1683 t
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Griffins, R. and Twari, B. Griffins, R. and Therr USE IN METHODS FOR SEX IDENTIFICATION IN
AVIAN GRIDS AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: WO 9639505-A 15 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
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Sequence 15 from Patent W09639505.
A58696
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1 (bases 1 to 6872)
Griffiths, R. and Korn, R.M.
A CHDI gene is Z chromosome linked in the chicken Gallus domesticus Gene 197 (1-2), 225-229 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF004397 6872 bp mRNA linear VRT 08-OCT-1997 Gallus gallus chromo-helicase-DNA-binding on the 2 chromosome protein, variant with hydrophilic domain, (CHD-2) mRNA, complete
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/gene="CHD-2"
/function="role in chromatin architecture"
/function="Cho protein with hydrophilic domain"
/codon_start=1
/product="chromo-helicase-DNA-binding on the Z chromosome
        PAT 06-MAR-1998
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Griffiths.R. and Korn.R.M.
Direct Submission
Submitted (16-7MX-1997) Zoology, Molecular Lab, Glasgow University,
Glasgow G12 8QQ, UK
                                                                                           unclessified.

unclessified.

Griffiths, R. and Tiwari, B.

AVIBM GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN

BIRDS
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        linear
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
1. .6608
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 Sequence 10 from Patent WO9639505.
A58691
A58691.1 GI:3714250
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/db_xref="taxon:9031"
1. .6872
                                                                                                                                                                                                                                                           /organism="unidentified"
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1207 c 1459 g 1653
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228. .5654
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AF004397.1 GI:2501845
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Best Local Similarity 91.39
Matches 94; Conservative
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SUBSESTEEROKSSCOGTSOTELDSOSOGNAMINANDELMAGNOSS FROUDS
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DEPTATORY STROATVANY SY REDEEMKTDSDDLLEVCGEDY POPEDEEFET ERVM
DCRVGRKGATGATT I I YAVEADGEDRAGTERNE FEGDIOY LIKWKGWSH HINWETEE
TLKQONVROMKKLLDNY KKROETKRALNANSPEDVEYYNCOGELTDDLIKQY OF YERI
I HABNOKSAAGLEDYY CKROGILP SECSWEDGAL I SKKFOT CIDEY FSROOSKTTPFK
DCKVLKORPFYALKKOPSY I GGHEGLELLYDY LONGLINMLAHSWCKGNSCI LADEMGL
GKTIOTI SPLANYLEHENQLY CSPLIAVY PLSTILTSWQREI QTWASOWNAVYLGILNSR
NAI THEMMHPOPIR RILKFNIILTTY EIILLKOKAFLGGILNMAFIGVDEAHRIK NDDSLL
YKTIIDF KSNHRLITTGTPLONSKELMENKENSPELLEN YKWELGENGSK
SCHKELEPPLLRRYKKCONGY LI KPPDNNEFYNKQEALOHLIRSK SKEGSK
GSTSGFLNIMMELKCCNHCY LI KPPDNNEFYNKQEALOHLIRSSSGKLIILLDKLLIRL
REGONYNLLISSONYMALDIILAFYK KROFSTEGENGKROALDIFFRANGSGEDF
CFLISTRAGGLGINLASARTVY YFEDSDWNPONDLOHLIRS STRELINGRALDHEN TROATVY TERSONYNYNYLLIR KRONTALTRYKKALDERGSEDF
CFLISTRAGGLGINLASARTVY YFEDSDWNPONDLOHLIRS STRELKRACALDHENGSGEDF
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Delmas, V., Stokes, D.G. and Perry, R.P.
A mammalian DNA-binding protein that contains a chromodomain and an Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
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SQSGSSDSDSGSDSGSQSESESDTSRENKVQAKPPKVDGAEFWKSSPSILAVQRSAML
RKQPQQAQQQRPASSNSGSEEDSSSSEDSDDSSGAKRKKHNDEDWQMSGSGSPSQLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Submission Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA on Feb 16, 1994 this sequence version replaced gi:293322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                      1159 AAGAAACCCCAGGCTAAGCAGTTACAGACTCGTGCAGATTACCTCATTAAATTACTGAAT 1218
                                                                                                                                                                                                                              52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
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0
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DNA binding protein.
                                                                  others
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                                                                                                                                             Score 87.6; DB 6;
Pred. No. 1.9e-15;
0; Mismatches 9;
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/protein_id="AAB08486.1"
/db_xref="GI:455015"
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/cell_type="plasmacytoma"
1. .5349
1. .1316
/organism="unidentified"
/db_xref="taxon:32644"
a 205 c 308 g 304
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/gene="CHD-1"
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91.2%;
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Matches 93; Conserv
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DAIARDAELVDKSEIDERLGELVHNOCVKALKDSSSGTERAGGELGKVKGPPFRISG
VQVNAKLVIAHEDELIPLHKSIPSDPERRKOYTIPGHTKAHFDIDMGKEDDSNLLIG
YQVNAKLVIAHEDELIPLHKSIPSDPERRKOYTIPGHTKAHFDIDMGKEDDSNLLIG
VETGYGGAGSKRRKTRAKSKAMKSITHKILDPDDFDKKRPAGKOLGTRADLIKLLSDDLAKREA
QRLCGAGGSKRRKTRAKKSKAMKSIKVKEETKSDSSPLDSRKSDEDDDKLNDSFPESK
DRSKKSVVSDAPVHITASGEPVPIAEESEELDOKTFSICKERMRPVKAALKQLDRPEK
GLSERQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKIWMIFVSKFTEFDARKLH
KLYKHAIKKROESQONSDONSVNATHVIRNDDMSRLKENTHHDDSSRDSYSSDRHLS
QYHDHHKDRHQEDSYKKSDSRKRPYSSFSNGKDHREWDHYRQDSRYYSDREKHKLLD
HRSREHRPSLEGGLKDRCHSDHRSHSDHRRHSDHRSSEHTHHKSSRDYRYLLSDWQLD
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                            ELEPERNSKNWEBIIPEEQRRRLEEEERQKELEBIYMLPRMRNCAKQISFNGSBGRRS
RSRRYSGSDSDSISERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLERL
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ELFKEPEGEEQEPQEMDIDEILKRAETHENEPGPLSVGDELLSQFKVANFSNMDEDDI
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257. .1939
/note="beta-gal fusion protein binds to blocks 10 to 3 of
HN fragment of delta-crystallin enhancer."
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
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Delta-crystallin enhancer binding protein delta EF1 is a zinc
finger-homeodomain protein implicated in postgastrulation
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delta-crystallin enhancer binding protein, complete sequence.
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1067 c 1319 g 1224 t
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80.2%; Pred. No. 5.7e-10;
tive 0; Mismatches 20;
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/tissue_type="lens"
/clone_lib="lambda gt11"
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Funchashi, J.
Unpublished (1994)
Location/Qualifiers
1. .2292
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Submitted (03-JUN-1997) Laboratory of Gene Transfer, National Human Genome Research Institutes of Health, 49
Convent Drive, Bethesda, MD 20892-4442, USA
Location/Qualifiers
                  LIRLRERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLÖGSIKGELRKQALDHFNAEG
SEDFCELLSTRAGGLINIASADTVVIFDSDMNPONDLÖAQARAHRIGGKKQVNIYRL
VYKGSVEEDILERAKKMYLDHLVIQRWDTTGKYVLHTGSTPSSSTPFNKEELSALLK
FGABELFREPGEEQDEQRAIDELLKARETRENEPGFUTVODELLSQFKVANTSOMD
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Home sapiens CHD1 mRNA, complete cds.
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Woodage,T., Basrai,M.A., Baxevanis,A.D., Hieter,P. and Collins,F.S. Characterization of the CHD family of proteins
Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
/translation-"MELKKCCNHCYLIKPPDDNEFYNKQEALQHLIRSSGKLILLDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                          53 AGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAATA 112
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                                                                                                                                                                                                                                                                                                                   10 44.6%; Score 68.2; DB 5; Length 2292; Similarity 85.4%; Pred. No. 9.8e-10; Conservative 0; Mismatches 13; Indéls 2.88; Conservative 0; Mismatches 13; Indéls 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 AAGACCTTGCAAGAAAAGAAGT--GCAAAGACTTACTGGTGCA 153
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1. .5947
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/db_xref="taxon:9606"
/chromosome="5"
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/gene="CHD1"
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Submitted (03-JUN-
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Matches 88;
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GLGKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSWQREIQTWASQMNAVVYLGDIN

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LYKTLIDEKSNHELITGTPLOALISELENDELSOALINGER GYGERENENDED
STARLEDER HAUT TRAINER THELL IT ELLENDER GYGYWHITTHENDED
YG STARLEDEPELLERVEKTOPER SLPARY BOLLINGERSALDKOYYWHITTHEN KALSEG
YG STAGETLIDMELKCCHHOTLIR PPDINEFY NROBALDKOYYWHITTHEN KALSEG
SKG STAGETLIDMELKCCHHOTLIR PPDINEFY NROBALDKOHLINGSGKLILLDKLLI
RLRERGNYH LIF SOWN RMLDILARY LKY RQPPORIDGAGARAH GGKKOWNY RLLY
KG SVEEDILERAK KWALDHLYI ORMOTTGKTVLHTGAR-SSTPFINEELSA ILKEG
AEELFERGES GEGEODGEMOLDETLIK RAFTHENE PGPLTVODELLAGFKVANFSINDED
BIELEPERNISK NWEEL IPPORRAK REELS YMLPRING KOLST SKENGSCR
BIELEPERNISK NWEEL IPPORRAK GERONT IP RENIK GFSDAETREFTS YN KERGEDLE
RLDAIARDAELVDK SEGTILREGELVHNGCIKALK DSSGTERTGRIKK VK RGPPLE
SCOYWARLY TSHEELELIPH KSIP DSDBERROYTT PRENIK GFSDAETREFTS YN KERDDSML
IG I PECTSGSWENIK RAMKSIK KILDDDDBKROOROGICARANDILIK LLESDLAKK
EALSGAGSSK RRRARAK KNAMKSIK VK KEIK SDSSPLPSEK SDEDDDKLSESK SDGR
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GLESREDGEHTROCLITATOHTECLKEYTPRDPOJKOKWRKINATIVSRFTEEDARKLH
KLYKHAIKKROSSOQNSDONSUNAPHYIRNPDVERLKEWTNHDDSSRDSYSSDRHLYO
YHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHRDWDHYKODSRYSDRENKLDDH
RSRDHINSNLEGSLKORGHSRDHRHJASDHRSSSEYTHHKSSRDYRYHSDWDWDH
RASSGCPREPLOKSYGSRSPFBHSHDHRLHSDHRSSSEYTHHKSSRDYRYHSDWDWDH
ARSSGCPREPLOKSYGSRSPFBHSVAR
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Direct Submission

Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Dec 7, 2001 this sequence version replaced gi:15290448.

Draft Sequence Produced by DOE Joint Genome Institute
SRNMIRTHEWTHHOTKRLKFNILLTTYEILLKDKAFLGGLNWAFIGVDEAHRLKNDDS
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1 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
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Db 118328 AGAGATCTTGCAAAAAAAGAAG 118349
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Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Second Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (Dases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-JTN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 134365)

DOE Joint Genome Institute and Stanford Human Genome Center.
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1 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                Db 26911 AAAAAACCACAAGCAAAACAGTTGCAGACCCGTGCAGCTACCTCATCAATTACTTAGT 26852
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Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mi
Drive, Walnut creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.
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Pred. No. 4.5e-09;
0; Mismatches 10;
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1. .101220
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-58M12"
a 18862 c 17827 g 30409 t
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/db_xref="taxon:9606"
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DOE Joint Genome Institute.
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(Sases I to 14307)

(Sanderson, S., Baldwin, J., Barna, W., Beckerly, R.,

(Bogualavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,

(Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

(Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

(Bardyna, S., Grant, G., Hagos, B., Haego, D., Galagan, J.,

(Gardyna, S., Grant, G., Hagos, B., Haego, M., Horton, L.,

(Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

(Landers, T., Lehoczky, J., Levine, R., Lieu, G., Liu, G., Locke, K.,

Macdonald, P., Marquis, N., Meswan, P., McGurk, A., McKernan, K.,

(McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,

(Norman, C.H., O'Connor, T., O'Donnell, P., Ollvar, T. M., Peterson, K.,

Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,

Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,

Direct Submission
AC021449 143079 bp DNA linear HTG 10-SEP-2000
Homo sapiens clone RP11-58M12, WORKING DRAFT SEQUENCE, 10 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 10, 2000 this sequence version replaced 91:7407963. All repeats were identified using RepeatMasKer: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143079)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L5154
Center clone name: 58_M_12
Center clone name: 58_M_12
Sequencing vector: M1s, M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 13743 bases at least Q40
Consensus quality: 139227 bases at least Q20
Consensus quality: 140814 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 141779; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens, clone RP11-58M12
                                                                                                                                    AC021449
AC021449.3 GI:10047806
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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38820: contig of 38820 bp in length

Oy 52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAAATTACTGAAT 111
Db 118268 AAAAAAACCACAAAAAAAGTTGCAGACCCGTGCAGACTACCTCATCAAATTACTTAGT 118327

112 AAAGACCTTGCAAGAAAGAAG 133

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Indels

Conservative

Matches

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Monatoria Sapiens

Homosapiens

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Consensus quality: 142556 bases at least Q30
Consensus quality: 143746 bases sum-of-contigs estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation.
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation.
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation.

** NoTE: This is a 'working draft' sequence. It currently
** consists of Toontigs. Gaps between the contigs
** is believed to be correct as given, however the sizes
** of the gaps between them are based on estimates that have
** provided by the submittor.
** This sequence will be replaced
** provided by the submittor.
** This sequence will be replaced
** the accession number will be preserved.
** by the finished sequence as soon as it is available and
** the accession number will be preserved.
** 100975 10374: contig of faffo by in length
** 113228 11327: contig of faffo by in length
** 113228 11327: contig of faffo by in length
** 113291 113294: contig of faffo by in length
** 113298 11327: contig of faffo by in length
** 113398 113397: contig of faffo by in length
** 113398 113397: contig of faffo by in length
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/clone=11b="CalTech human BAC library C"
/clone_11b="CalTech human BAC library C"
26309 c 27580 g 48609 t 600 others
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center Project Name: 369535
Center clone name: CIT-HSPC_480Bl1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.jgi.doe.gov
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Best Local Similarity
Matches 72; Conserv
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SOURCE
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Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE,
7 ordered pieces.
ACO08531 GI:12830078
HTG; HTGS_PHASE2; HTGS_DRAFT.
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Db 116168 AAAAAACCACAAGCAAAACAIIGCAGACCGGIGCAGACTACCICAICAAAIIACIIAGI 116227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143079: contig of 36570 bp in length. Location/Qualifiers
          38921 38920: gap of 100 bp 38921 40411: contig of 1491 bp in length 40421 2011: gap of 100 bp 40512 43279: contig of 2768 bp in length 43280 43379: gap of 100 bp 45906 47005: gap of 100 bp 46905: contig of 4825 bp in length 47006 51830: contig of 4825 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11=58M12"
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1. 38820
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43971 a 26246 c 26678 g 45278 t
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/A066. 251830
/A066. 251830
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/A066. 251830
/A066. 25280
/A066. 2536mbly_fragment"
62720. 75408
/A066. 2536mbly_fragment"
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76500. 143079
/A066. 2536mbly_fragment
clone_end:Theorem
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38921. .4041.
/note-"assembly_fragment"
40512. .43279
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43380, 46905
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ACCESSION VERSION KEYWORDS

SOURCE

AC091946

RESULT

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AUTHORS JOURNAL

COMMENT

unknown 4585

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/clone="RP11-36012"
/clone_lib="RPCI human BAC library 11"
1 35252 c 37061 g 60360 t 3202 others
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130583: contig of 6745 bp in length
130683: gap of unknown length
141544: contig of 10861 bp in length
141644: gap of unknown length
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Consensus quality: 180759 bases at least Q30
Consensus quality: 180759 bases at least Q30
Consensus quality: 180759 bases at least Q30
Consensus quality: 184175 bases at least Q30
Consensus quality: 184175 bases at least Q30
Consensus quality: 184175 bases stimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fpe stimation
Quality coverage: 5.78 in Q20 bases; aum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                               AC091946 193446 bp DNA linear HTG 09-JUN-2001
Homo sapiens chromosome 5 clone RP11-36012, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 193446)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5
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Center Project Name: 544799
Center clone name: RPCI-11_36012
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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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of 27465 bp in length

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                                               Gaps
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              43.1%; Score 66; DB 2; Length 193446; 87.8%; Pred. No. 4.5e-09; ive 0; Mismatches 10; Indels 0
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AC104132 Homo sapi
AL162390 Human DNA
AC100856 Homo sapi
AC018358 Homo sapi
AC018358 Homo sapi
AC08594 Homo sapi
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AC645938 Mus muscu
X58562 C.porcellus
AF059650 Homo sapi
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Other publication AU 5906996 961224.
Location/Qualifiers
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Consensus quality: 154414 bases at least Q40
Consensus quality: 183510 bases at least Q30
Consensus quality: 184856 bases at least Q30
Consensus quality: 194886 bases at least Q30
Consensus quality: 194886 bases at least Q30
Estimated insert size: 23310; sum-of-contigs estimation
Estimated insert size: 233130; sum-of-contigs estimation
Quality coverage: 3.7 in Q20 bases; squeose:fp estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 61 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
2 (bases 1 to 239130)
Direct Submission
Direct Submission
Submitted (01-SEP-2000) Production Sequencing Facility, DOE Joint
Schome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                        contig of 1030 bp in length
gap of unknown length
contig of 1390 bp in length
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Center clone name: RPCI-23_104L12
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151374: contig of 8722 bp in length 151374: contig of 8722 bp in length 159603: contig of 8129 bp in length 159503: contig of 8129 bp in length 169275:
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Mammalla; Eutheria; Rodentia; Sciurognathi; Murlaes; Murinae;
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* 195252 204073: contig of 8822 bp in length

* 204074 204173: gap of unknown length

* 217102 217201: gap of unknown length

* 217702 217201: gap of unknown length

* 217302 227352: contig of 10151 bp in length

* 277353 227452: gap of unknown length

* 277453 227452: gap of unknown length

* 277453 239130: contig of 11678 bp in length

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* (chorelnites = "taxon: 10090" | chromosome="16" | chromoso
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Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 32; Conservative 0; Mismatches 0;
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NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Tamerisa, K. Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Ward, Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, R., Waelley, K., Wu, C., Wu, Y., Williamson, A., Wleczyk, R., Wooden, S., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                     Submitted (25-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Dec 20, 2001 this sequence version replaced gi:17064227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 82281 bases at least Q40
Consensus quality: 8876 bases at least Q30
Consensus quality: 94579 bases at least Q20
Estimated insert size: 78830; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length
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------ Summary Statistics
Assembly program: Phrap; version 0.990329First call to
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Contact: hgsc-help@bcm.tmc.edu
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19218:
22751:
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41552
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43299
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45055
                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                         TITLE
JOURNAL
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Matches

RESULT 4 AC091404

ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

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Mus musculus
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        32724
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                                                                                                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENKATYOCA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ENKATYOCA; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

E. 1 (bases 1 to 158755)

S. Ayele, K., Beckstrom-Sternberg, S.W., Benjamin, B., Blakesley, R.W., Buoffata, G.G., Birinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Ho, S.-L., IGOLJ, R., Karlins, E., Lee-Lin, S.-Q., Legaspi, R., Lim, M., Maduro, C.L., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Suyder, B., Stantripop, S., Thomas, J.W., Thomas, P.J., Tlongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., NISC Comparative Sequencing Initiative

L. Unpublished
                                                                                                                                                                                                                                                                     HTG 19-APR-2001
                                                                                                                                                                                                                                                                     ACO91404 158755 bp DNA linear HTG 19-APR-20
Sus scrofa clone RP44-74011, WORKING DRAFT SEQUENCE, 6 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-APR-2001) NIH Intramural Sequencing Center, 8717 Growmont Circle, Galthersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing the statistics Sequencing vector: plasmid; NAVILI Sequencing vector: plasmid; nAs: 100% of reads Sequencing vector: plasmid; nAs: 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 15545 bases at least Q40
Consensus quality: 155545 bases at least Q20
Consensus quality: 156572 bases at least Q20
Consensus quality: 156597 bases at least Q20
Insert size: 156000; pulse-field-gal
Insert size: 188025; sum-of-contigs
Quality coverage: 10.68x in Q20 bases; pulse-field-gal
Quality coverage: 10.39x in Q20 bases; sum-of-contigs
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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        Length 100325;
                                                    Indels
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3349: app of unknown length
13662: contig of 9913 bp in length
31762: app of unknown length
32623: contig of 18861 bp in length
32723: app of unknown length
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4.3%; Score 31; DB 2; Le
100.0%; Pred. No. 7.8e-06;
'ative Q; Mismatches O;
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AC091404.1 GI:13677075
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                                                    31; Conservative
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     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                     AC091404
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TITLE JOURNAL

COMMENT

REFERENCE

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Debritain to 161092)

Shirten, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Barnen, B., Linton, L., Camparata, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Gorde, P., P. Fitzhuph, W., Gage, D., Galagan, J., Gardyna, S., Gilde, S., Gold, S., Goyette, M., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Jones, C., Kamat, A., Karatas, A., Kells, C., Lascoque, K., Lu, G., Langares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Liu, G., McCarthy, M., WcEwan, P., McKernan, K., McPheeters, R., Mihova, T., Whonga, V., Murphy, T., Naylor, J., Naylor, C., Norman, C., H., O'Connell, P., O'Donnell, P., O'Nell, D., O'Donlall, P., O'Donlar, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS CLONE RP24-192F16, WORKING DRAFT SEQUENCE, 13 UNDOCACHE Dieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 161092) Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-192F16
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75771: gootig of 22448 bp in length
25771: goo of unknown length
28557: contig of 31096 bp in length
88647: goo of unknown length
18 15875: contig of 72288 bp in length
Location/Qualifiers
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HTG; HTGS_PHASE1; HTGS_EDRAFT; HTGS_FULLTOP.
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4.3%; Score 31; DB 2;
Best Local Similarity 100.0%; Fred. No. 7.5e-0
Mismatches
7.5e-0
Mismatches
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41826 a 38951 c 37930 g 39519 t
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13763. 32623
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32724. 55171
/note-"assembly_fragment
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86468. .158755
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                                                                                                                                                                                                                      /organism-"Sus scrofa"
                                                                                                                                                                                                                                                   /db_xref-"taxon:9823"
                                                                                                                                                                                                                                                                                   /clone="RP44-74011"
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3750. .13662
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55272. .86367
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1. .3649
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Query Match
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AUTHORS
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Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Steaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N. Strauss, M., Subramanian, A., Talamas, J., Tresfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triquilo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zannoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Search, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatWasker.html
                                                                                                                                                                                                                                                                                                                                                                             ......Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Conter project Information
Center project name: 1170.
Center clone name: 192_F_16
Center clone name: 192_F_16
Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 158076 bases at least Q40
Consensus quality: 15807 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 157000; agarose-fp
Insert size: 159992; sum-of-contigs
Quality coverage: 8.8 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127911 128010: gap of 100 bp 128011 149944; contig of 21934 bp in length 19945 150044; gap of 100 bp 150045 161092; contig of 11048 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53: gap of 100 bp 68690: contig of 40337 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109434 109533: gap of 100 bp
109534 127910: contig of 18377 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9908 10007: gap of 100 bp
10008 11803: contig of 1796 bp in length
11804 11903: gap of 100 bp
11904 14164: contig of 2261 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14165 14264: gap of 100 bp 14265 16540: contig of 2276 bp in length 16541 16640: gap of 100 bp 16641 18624: contig of 1984 bp in length 18625 18724: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24: gap of 100 bp 105.253: contig of 3869 bp in length 100 bp 105.253: contig of 5860 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9907: contig of 9907 bp in length
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/clone="RP24-192F16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
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18725 2229
22294 22393:
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misc_feature

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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Adio. Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbases I to 162071)

Muzny, D.M., Adams, C., Adio-Oduola, B., Balis, T., Banks, T., Banks, T., Banks, T., Banks, T., Banks, T., Banks, T., Buck, J., Bouck, J., Bouck, J., Blankenburg, K., Bonnin, D., Bouck, J., Burdet, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, Z., Chowdhry, J., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Dalgado, O., Dan, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Farrant, C., Edgar, D., Edwards, C.C., Elhaj, C., Esottch, M., Falls, T., Ferrant, C., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Harris, C., Howait, S., Hune, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC096932 162071 bp DNA linear HTG 21-DEC-2001 Rattus norvegicus chromosome Renin clone CH230-57H13, *** SEQUENCING IN PROGRESS ***, 66 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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... Pred. No. 7.5e-06;
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44315 a 34609 c 34525 g 46427 t
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// 28354. 68690
// note="assembly_fragment"
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18725 .22293
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AC096932.3 GI:17975665
HTG; HTGS_PHASE1.
                                                         11904. .14164
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Matches 31; Conservative
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Rattus norvegicus
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us-08-973-363-1.oli.rge

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130640:
130740:
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64604:
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Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kartovic, J., Kureshi, A., Leadis, M., Leal, B., Lewis, L., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Marinez, E., Massey, E., Marhiney, E., Martinacie, A., Martinacie, M., Ren, Y., Rives, M., Rolssa, A., Stanley, H., Ovledo, R., Pacce, A., Paton, B., Oulies, M., Ren, Y., Rives, M., Robas, A., Stanley, H., Stanch, J., Savery, G., Saherer, S., Scott, G., Shen, H., Shooshtari, N., Stanley, H., Sutton, A., Svatek, A., Tang, H., Tansey, M., Vasquez, L., Varca, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Wartek, A., Tang, H., Wang, S., Wartek, A., Tang, Wartington, S., Walliams, G., Walliamson, A., Wachington, C., Walliams, G., Walliam, Mang, S., Wartek, M., Walliam, Mang, S., Walliam, Mang, S., Walliam, Mang, S., Wall
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NOTE: This is a "vorking draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 128926 bases at least Q40
Consensus quality: 136110 bases at least Q30
Consensus quality: 142174 bases at least Q20
Estimated insert size: 129055; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fip estimation
quality coverage: 2.4x in Q20 bases; sum-of-contigs estimation
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8187: gap of unknown length
1670: contig of 8583 bp in length
16870: gap of unknown length
21956: contig of 5086 bp in length
26652: contig of 5086 bp in length
2652: contig of 4596 bp in length
26752: gap of unknown length
26752: gap of unknown length
26752: gap of unknown length
26753: gap of unknown length
26753: gap of unknown length
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gap of unknown length
contig of 5016 bp in length
gap of unknown length
contig of 4191 bp in length
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31; Conservative
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Plumb, B.
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AUTHORS
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                                               FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169467 bp DNA linear HTG 08-FEB-2002 et 4 clone RP23-306F22, *** SEQUENCING IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 4, 2002 this sequence version replaced gi:18477372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGRP4; version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 169431 bases at least Q40
Consensus quality: 169464 bases at least Q20
Insert size: 169467; sum-of-contigs
Unsert size: 162312; 10.1% error; agarose-fp
Quality coverage: 11.88x in Q20 bases; sum-of-contigs Quality
coverage: 12.40x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                            contig of 1713 bp in length
gap of unknown length
contig of 1176 bp in length
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gap of unknown length
contig of 1194 bp in length
                                                                                                                        of 2284 bp in length
unknown length
of 1534 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                    7.5e-06;
nes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Wellcome Trust Sanger Institute
                                                                                                                        contig of 2284 b
gap of unknown l
contig of 1534 b
gap of unknown l
contig of 1429 b
gap of unknown l
gap of unknown l
contig of 1010 by
gap of unknown l
gap of unknown l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 144352 CCACTCTTTTTTTTTTTTTTTTTTTTTTTGGC 144322
                                                                              unknown
of 1893
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.3%; Score 31; DB Best Local Similarity 100.0%; Pred. No. 7.5 Matches 31; Conservative 0; Mismatches
                                                                                                           unknown
                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 CCACTCTTTTTTTTTTTTTTTTGGC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus chromosome 4 clone
PROGRESS ***, in ordered pieces
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contig
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gap of
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gap of
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145956:
146056:
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134940:
136833:
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142380:
142480:
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140952
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Hammond, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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170536 bp DNA linear PRI 04-FEB-2002
Homo sapiens chromosome 9 BAC RP11-518K17, complete sequence.
AL513423 AL533720
AL513423.2 GI:18539155
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Submitted (07-FEB-2001) GBF, Dept. of Genome Analysis, Mascheroder
Weg 1, D-38124 Braunschweig, Germany, E-mail: info.genome@gbf.de
On Feb 5, 2002 this sequence version replaced gi:12718191.
All annotations in this database entry are developed by
computational tools. It is therefore not explicitly noted in the
feature lines that evidence is not experimental.
Mapping was performed at The Sanger Centre
(cf. http://www.sanger.ac.uk/HGP/Chr9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (09-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: cloneraguest@sanger.ac.uk
(bases 1 to 170536)
Scharfe,M., Conrad,A., Hornischer,K., Loehnert,T.H., Thies,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata, Craniata, Vertebrata, Euteleostomi,
Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://webace.sanger.ac.uk/cgi-bin/display?db=acedb9&grep=518K17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                   by the finished sequence as soon as it is available and the accession number will be preserved.

Location/Qualifiers
1. 169467
/organism="Mus musculus"
/db_xref="taxon:10090"
//chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 169467;
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Chemistry: Dye-terminator-amersham: 55% of reads
Chemistry: Dye-trimer-amersham: 12% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 0 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                                                                          4.3%; Score 31; DB 2; Len
Pred. No. 7.5e-06;
                                                                                                                                                                                                                                 /clone_lib="RPCI-23"
1. .169467
/note="assembly_fragment:04690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mapping information is available via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 58711 ACTCTTTTTTTTTTTTTTTTTTTTTGGCTT 58681
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Contact: info.genome@gbf.de
                                                                                                                                                                                                                                                                                                                                          vector_side:left"
a 39075 c 37946 g 45672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    445 ACTCTTTTTTTTTTTTTTTTTTTGGCTT 475
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* This sequence will be replaced
                                                                                                                                                                                                           /clone="RP23-306F22"
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Center code: GBF
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                                                                                                                                                                                                                                                                                                                       clone_end:SP6
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Mammalia; Eutheria;
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/rpt_type=TANDEM
10318. 10457
/orte="GRAIL, score = 70%, comment = good shadow"
complement(10763. 10799)
/note="GRAIL, score = 77%, comment = excellent"
11782. 11861
/note="GRAIL, score = 47%, comment = marginal shadow"
complement(12003. 12016)
/note="GRAIL, score = 47%, comment = marginal shadow"
/note="GRAIL, score = 47%, comment = marginal shadow"
/note="Spoin"
/note="homology = 82.7%, counts = 26"
/rpt_type=TANDEM
/rpt_type=TANDEM
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/note-12059
/note-12059
/note-family="L1"
/rpt_family="L1"
/note-inonlogy = 70.1%, counts = 7"
/rpt_family="agaaagcaaga repeat"
                                complement(2225. .6898)
//note="94% identity: matches 1344. .6024 of consensus"
//pt_maily="L1"
| 1545. .2582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // Instance = Constance = Cons
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700te **XPOUND prediction, score = 0.349"

complement(7586 . 8358)

7note **93% identity: matches 7. .776 of consensus **

/rpt_family **L1**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="GRAIL, score = 51%, comment = good 7964. B094
/note="XPOUND prediction, score = 0.547"
complement (8287. 8340)
                /rpt_family="atattatttttttttttttttrrpeat"
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12927. .12937
                                                                                                     repeat_region
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"Tradem Repeats: GDE 2.2 option 'tandam'

"Indimum length 2 bp; Maximum length 20 bp; Score threshold 20.

Tract N's as mismatches? YES: Allow uniform consensi? NO >
'Inverted Repeats': GDE 2.2 option 'inverted' (Abajian) > 'CpG
Islands': GDE 2.2 option 'sputnik' (Abajian) > 'CpG
Islands': GDE 2.2 option 'sputnik' (Abajian) > 'CpG
Islands': GDE 2.2 option 'sputnik' (Abajian) > 'CpG
Islands 'GDE 3.2 option 'Sputnik' (Abajian) > 'CpG
Island region size 100 bp;

Minimum GC contents 50 %; Observed/Expected 0.6 > 'STS Scan':
e-PCR (Schular)

"Margin: 50; Number of mismatches allowed: 0; Word size: 7 .
STS database: 'GDSTS markers'
> 'tRNA Scan': tRNAscan-SE [Lowe & Eddy), Vers: 1.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior probability: 0.04; Overlapping number: 0 > Xpound (Thomas
                                                                                                                                                                                                                                                                                                                       /dironsome="9" //dironsome="9"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1390. .1427

/note="INIVERFED" 76% complementary to IR1' (2545. .2582)" /rote="INVERFED" 2114. .2233 //ote="homology = 66.7%, counts = 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368. .415
/note="95% identity: matches 177. .224 of consensus"
/rpt_family="L1"
1012. .1023
Consensus quality: 0 bases at least Q30 consensus quality: 0 bases at least Q30 Estimated insert size: ##; agarose-fp estimation Estimated insert size: ##; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        > GenScan (Burge & Karlin), Vers. 1.0
Used matrix: vertebrate; Minimum score: 0
Grail (Yu et al.), Vers. 1.3
Organism: human
> Mzef (Zhang)
                                                                                                                                                                                                                                      PROGRAMS AND PARAMETERS USED FOR ANNOTATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="TA repeat"
1390. 1407
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/note="AT repeat"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 18238)

Eujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

L. (bases 1 to 18238)

E. (bases 1 to 18238)

E. Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

E. Submitted (05-APR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

I.7-22 Suehiro-chou,Tsurumi:Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattorieggs:riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tal:81-45-503-9111, Fax:81-45-503-9170)

On Jan 22, 2001 this sequence version replaced gi:10130043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 9 clone RP11-778P13, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
Rameay, H.

Direct Submission

Submitted (24-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: hundquery8sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced gi:18181754.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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4.3%; Score 31; DB 9; Length 182328;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 31; Conservative 0; Mismatches 0; Indels 0
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/db_xref="taxon:9606"
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Homo sapiens chromosome 5 clone CTC-210G5, complete sequence.
ACO22101
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DOE Joint Genome Institute.

DOE Joint Genome Institute.

Submitted (26-1AM-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 10 (Dases I to 173691)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (29-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 29, 2001 this sequence version replaced gi:7711682.

Draft Sequence Produced by DOE Joint Genome Institute
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1 (bases 1 to 173691)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
            /note="GRAIL, score = 91%, comment = excellent shadow" complement(15145. .15418)
/note="81% identity: matches 312. .587 of consensus" /rpt_family="L1"
15147. .15418
/note="84% identity: matches 11. .281 of consensus" /rpt_family="ALU"
/rpt_family="ALU"
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tive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                          4.3%; Score 31; DB 9; Length 170536; 00.0%; Pred. No. 7.5e-06;
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Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
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Estimated Total Number of Errors is 0.2.
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Center: Whitehead Institute/ MIT Center for Genome Research
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: Wabs
Web site: http://www.seq.wi.mit.edu
Web site: http://www.seq.wi.mit.edu
Centert: sequence_submissions@genome.wi.mit.edu
Centert: project Information
Center project name: 13279
Center clone name: 256_2_1

Sequencing vector: Plasmid: n/a: 100% of reads
Assembly program: Phrag) vector: Plasmid: n/a: 100% of reads
Assembly program: Phrag) vector: Plasmid: n/a: 100% of reads
Assembly program: Phrag) vector: plasmid: n/a: 100% of consensus quality: 238849 bases at least Q30
Consensus quality: 238849 bases at least Q30
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Consensus quality: 238840 bases at least Q30
Consensus quality: 238842 bases at least Q30
             Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (Je-Aud-2001) Whitehead Institute/MIT Center for Ger
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-11997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently
consists of 11 contigs. The true order of the pleces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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12397: contig of 12397 bp in length
12398 12497: gap of
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13992 13991: gap of
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18661 1860: gap of
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29926 48714: contig of 100 bp
48715 48814: gap of
48715 48814: gap of
11227 112326: contig of 63412 bp in length
11227 12366: contig of 63412 bp in length
11227 12366: contig of 6342 bp in length
11227 12366: contig of 6342 bp in length
11217 13986: contig of 3336 bp in length
11387 12865: contig of 3336 bp in length
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/db_xref="taxon:10090"
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12498. .13891
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Mus musculus clone RP23-256C1, WORKING DRAFT SEQUENCE, 11 unordered
pieces.
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Consensus quality: 199198 bases at least Q40 Consensus quality: 199267 bases at least Q30 Consensus quality: 199325 bases at least Q20 Insert size: 199311; sum-of-contigs Insert size: 189316; 8.7% error; agarose-fp Quality coverage: 16.0% in Q20 bases; sum-of-contigs Quality coverage: 15.0% in Q20 bases; sum-of-contigs Quality
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* This sequence will be replaced
* Dy the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
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clone_end:SP6
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| 36635 c 39266 g 65103 t
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/db_xxef="taxon:9606"
/chromosome="9"
/clone="RP11-778P13"
/clone="RP11-778P13"
1. .199311
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8820 9511: cor
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8719:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 65400)
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Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mus musculus clone RP23-279P3, LOW-PASS SEQUENCE SAMPLING.
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53178 c 53976 g 65866 t
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219966. .240682
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                                                                                                            48815, .112226
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Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                      9822 9611: Control of 0.0 bp

9612 10326: Control of 0.0 bp

10327 10426: gap of 100 bp

10427 11119: Control of 693 bp in length

1120 11219: gap of 100 bp

1120 11219: gap of 100 bp

1120 11296: Control of 693 bp in length

1120 1219: gap of 100 bp

12037 12036: gap of 100 bp

12037 12036: gap of 100 bp

12037 12039: control of 694 bp in length

13524 13623: gap of 100 bp

13624 14325: Control of 695 bp in length

1436 14325: Control of 696 bp in length

1426 15121: control of 696 bp in length

15122 15211: gap of 100 bp

16022 16021: gap of 100 bp

16022 16714: control of 693 bp in length

16715 16814: gap of 100 bp

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19103: contig of 705 bp in length
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of 702 bp i
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ó; Query Match Best Local Simi Matches 30;

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21571 21670: gap of 100 bp 22354: contig of 684 bp in length 22355 22454: contig of 684 bp in length 22355 22454: contig of 6700 bp in length 23355 22454: gap of 100 bp 23355 2345; gap of 100 bp in length 24046 24055: contig of 610 bp in length 24056 24825: contig of 710 bp in length 24056 24825: contig of 710 bp in length 25536 contig of 688 bp in length 25536 contig of 688 bp in length 27044 27243: gap of 100 bp in length 27047 28056: gap of 100 bp in length 28059 28058: contig of 688 bp in length 28059 28058: contig of 688 bp in length 28047 2916: contig of 682 bp in length 28047 2918: gap of 100 bp in length 28048 2918: gap

RESULT

AC102249

HTG; HTGS_PHASEO.

AUTHORS TITLE REFERENCE

Unpublished JOURNAL REFERENCE

is contig of 716 bp in length app of 100 bp is contig of 707 bp in length ap of 100 bp in length is contig of 699 bp in length

36712 36811: gap of 10 36812 37518: contig of 7 37519 37618: gap of 10 37619 38317: contig of 6

35995: gap of 36711: con

38318 38417: gap of 100 bp 38418 39125: contig of 708 bp in length

oof 100 bp contig of 694 bp in length p of 100 bp contig of 699 bp in length oof 100 bp contig of 695 bp in length

39225: gap of 39919: cont 40019: gap of 40718: con 40818: gap of 41513: con 41613: gap of 42307: cont

TITLE COMMENT Center: Whitehead Institute/ MIT Center for Genome Research

47977; gap of 100 bp 4674. contig of 697 bp in length 48774; gap of 100 bp 49470; contig of 696 bp in length 49570; gap of 100 bp 50263; contig of 693 bp in length 50363; gap of 100 bp

19471 49570:

Center project name: L18261

ALE Dipublished

RE Birren.B. Lintcon.L., Nusbaum,C., Lander.E., Ali,A., Allen.N.,

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Raderson.S., Barnan.N., Bastien.A., Chang.J., Chazaro,B.,

Brown.A. Camarata.J., Canpoplano.A., Chang.J., Colaymore.A., Cook.A.,

Cockepel.Y., Colangelo.M., Collins,S., Collymore.A., Cook.A.,

Cooke,P., DeArellano.K., Dewar,K., Didaz.J.S., Dodge.S., Faro,S.,

Ferreira.P., FitzHugh,M., Gage,D., Galagan.J., Gardyna.S.,

Ginde,S., Gord.S., Goyekte,M., Graham.L., Garand-Pierre.N.,

Hagos,B., Heaford.A., Horton.L., Hulme.W., Illev.J., Johnson.R.,

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Lamazares,R., Landers.T., Lehoczky.J., Marquis,N., Matthews,C.,

MacCarthy,M., McEwan.P., McKernan.K., McPheeters,R., Meldrim.J.,

Meneus.L., Mihova.T., Mlenga.V., Wurphy.T., Naylor.J., Naylor.J., Norwic.C.,

Oliver.J., Peterson.R., Phueckan.N., Pollara.V.,

Raymond.C., Retta.R., Ribback,M., Riley. Pierre.N., Pollara.V.,

Raymond.C., Retta.R., Taleback,M., Saltcs.R., Schupback,R.,

Seaman.S., Severy,P., Spencer.B., Stanger-Thoman.N., Stojanovic.N.,

Strauss.N., Subramanian.A., Talamas.J., Tesfaye,S., Theodore.J.,

Viel.R., Vo.A., Wilson.B., Wu.X., Wyman.D., Ye,W.J., Young,G.,

Zainoun.A., Zembek,L., Zimmer.A. and Zody.M.

Direct Submission

Research, 230 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker: html

Litp://fip.genome.washington.edu/RW/RepeatWasker.html MUS MUSCULUS CLONE RP24-160D21, LOW-PASS SEQUENCE SAMPLING. AC102249 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 67166) Gaps Length 65400; 50364 51056: contig of 693 bp in length 51157 51156: gap of 100 bp 51157 51863: contig of 707 bp in length 51864 51963: gap of 100 bp 61964 52773: gap of 100 bp 61964 52773: gap of 100 bp 619774 53488: contig of 715 bp in length 53489 53589 54302: contig of 714 bp in length 5430 54403 55110: contig of 708 bp in length 55111 55210: gap of 100 bp 4.1%; Score 30; DB 2; Length 654 Similarity 10.0%; Pred. No. 2.7e-05; 80; Conservative 0; Mismatches 0; Indels Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-160D21 449 TTTTTTTTTTTTTTTTTTTTGGCTTCTT 478 AC102249.1 GI:17061335 house mouse. Mus musculus AUTHORS

DEFINITION ACCESSION KEYWORDS

ORGANISM

ap of 100 bp 100

gap of 43099:

42407

43199: gap of 43905: con 44005: gap of 44716: con

p of 100 bp contig of 711 bp in length p of 100 bp contig of 662 bp in length

o of 100 bp contig of 710 bp in length

45479 45578: gap of 45579 46288: con

44816: gap of 45478: con

o of 100 bp contig of 692 bp in length

con. 47080:

30: gap of 100 bp 47877: contig of 697 bp in length

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87 3186; gap of 100 bp 13856; contig of 670 bp in length 13956; gap of 100 bp 110 bp 111 34710; gap of 100 bp 111 35382; contig of 672 bp in length 138782; contig of 672 bp in length 135482; gap of 100 bp 
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26176: contig of 690 bp in length
26276: gap of 100 bp
27048: gap of 100 bp
27048: gap of 100 bp
27699: contig of 651 bp in length
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24616: contig of 666 bp
116: gap of 100 bp
25386: contig of 670 bp
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44704
44804
                                                                                                       * NOTE: This record contains 87 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* dentifying clones that may be gene-ritch and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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contig of 689 bp in length
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contig of 684 bp in length
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Center clone name: 160_D_21
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.: gap of
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4526 //
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8466: con
78566: gap of
9248: con
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6108:
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6109
6209
6897
6897
7686
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8467
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638 bp in length

TYPE STATE

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identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7785; gap of 100 bp in length 9248; contig of 681 bp in length 100 bp 10
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25386; contig of 670 bp in length
25486; gap of 100 bp in length
26176; contig of 690 bp in length
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10021: contig of 673 bp in length
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Mus musculus clone RP24-160D21, LOW-PASS SEQUENCE SAMPLING.
AC102249
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Bukaryota; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 67166)
Birrach B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-160D21
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Smit. A.F.A. & Green, P. (1995-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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51755 52429: contig of 675 bp in length
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2.7e-05;
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TITLE
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38447; contig of 699 bp in length 38548  
39220; contig of 673 bp in length 39221  
39221 39320; contig of 673 bp in length 39221  
39221 39320; cap of 100 bp  
39321 40006; contig of 686 bp in length 40007 40106; gap of 100 bp  
40107 40795; contig of 689 bp in length 40895  
40895 639 po of 100 bp  
41567 41666; gap of 100 bp  
41667 4266; gap of 100 bp  
4264 42463; gap of 100 bp  
42464 43127; contig of 664 bp in length 43128 4327; gap of 100 bp  
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43128 4327; gap of 100 bp  
43198; contig of 691 bp in length 43918; contig of 685 bp in length 44018; gap of 100 bp  
44019 44703; contig of 685 bp in length 4568; gap of 100 bp  
44019 44703; contig of 655 bp in length 4569 4558; gap of 100 bp  
44019 44703; contig of 670 bp in length 4569 4558; gap of 100 bp  
4712; gap of 100 bp  
4718; 47883; gap of 100 bp  
4718; 47883; gap of 100 bp  
4718; 47883; contig of 671 bp in length 4783; contig of 671 bp in length 4784; 47883; gap of 100 bp  
47644 4864; 4865; gap of 100 bp  
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26177 26276: gap of 100 bp 26948: contig of 672 bp in length 26949 27699: contig of 651 bp in length 27699 27699: contig of 651 bp in length 27700 27699: contig of 651 bp in length 27700 27799: gap of 100 bp 27800 28668: contig of 665 bp in length 28469 29233: contig of 665 bp in length 30005: contig of 672 bp in length 30006 30077: contig of 672 bp in length 30168 3087: gap of 100 bp 20153: contig of 672 bp in length 30168 3087: gap of 100 bp in length 31523: contig of 673 bp in length 31524 31523: contig of 673 bp in length 31529 32396: contig of 673 bp in length 31529 32396: contig of 673 bp in length 31887 3386: contig of 670 bp in length 31887 3386: contig of 670 bp in length 31887 3386: contig of 670 bp in length 31887 34610: contig of 672 bp in length 31813 35482: gap of 100 bp in length 35481 35482: gap of 100 bp in length 35483 35482: contig of 661 bp in length 36243: gap of 100 bp in length 36347: contig of 667 bp in length 36347 37788: gap of 100 bp in length 36342 37778: gap of 100 bp in length 36343 37778: gap of 100 bp in length 36343 37778: gap of 100 bp in length 36344 36513: contig of 665 bp in length 36778 gap of 100 bp in length
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DB 2; Length 67166;

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Query Match

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Human ORFX ORF2416
Human colon cancer
Human breast cance
Human breast cance
Human immune/haema
Human secreted pro
Human secreted pro
Human endocrine po

ļņ

Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny

Tiwari B;

Griffiths R,

& Query Match

Score

Result No.

1000 0.04 0.44 0.44 0.86 0.86 0.86 0.86 0.86

72222222

WPI; 1997-043127/04.

Human immune/haema cDNA nfSPI7-549 en Complementary stra Human ORFX ORF2416 ~

standard; cDNA; 429

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 gttgtgtgttttgaggaaaaataaaatgtttaagttgtccattccttgaaacctcccgacc 720
                                                                                                                                                                                                                                                                                         481 TATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAGTTTGGTTTCCCTGTCACTGTTTTCTTTCCTTGAAACTGACTTTCATTTGCAACATG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTGCCAAACTGTAGCTTTGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 catttagggaaatactggagtgaagcaaacacagtggtactgccaaactgtagctttggg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                          putative exon was isolated of a gene that was designated CHD-W due to its close identity to the mouse CHD-1 gene and its W location. This CHD-W fragment was used to isolate a similar gene (see also AAT42751) from chicken. This gene was not W-located, and was named CHD-1A. A second, W-located chicken gene (CHD-W) closely related to CHD-1A was also identified (see also AAT42754). The CHD-1A and CHD-W genes are useful for bird sex determn.
                     {\tt GT-W} (AAT42755) was cloned from a W chromosome specific PCR it derived from great tit. It represents part of an intron in inked gene. By moving downstream from this sequence, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGGTCGGAGGTTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGAC
                                                                                                                                                                                                                                                                                                                                                                                 361 ATTIGAGGAGCCACAGAGTIGIATAIAAAITIGITIAAIGAIAICCIGCCCCIGCCTICC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 ATGACAGTGGTACAGGAGCTCTGAATTTTTTAGATAAACTATGAGAGTGGAAACAGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 ctgaggctagtttcttgagctgactgtaaattttgtgagaatattttcaagactacatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTGTGTGTTTGAGGAAAAATAAAATGTTTAAGTTGTCCATTCCTTGAAACCTCCCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                    Length 723;
                                                                                                                                                                                                            Indels
                                                                                                                                                  Sequence 723 BP; 188 A; 109 C; 164 G; 262 T; 0 other;
                                                                                                                                                                                    100.0%; Score 723; DB 18; 100.0%; Pred. No. 1.2e-280;
                                                                                                                                                                                                           0
                                                                                                                                                                                                           0; Mismatches
8; Fig 1; 76pp; English.
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                Similarity
                                  product derived f
a W-linked gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         723
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                                                                                                                                                                                                           723;
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                                                                                                                                                                                                 Local
 Claim
                                                                                                                                                                                                Best Loca
Matches
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, immunomodulatory activities activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful. In the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   part of the printed directly from WIPO
                                                                                                                                                 proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                      vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides, useful for preventing y. Leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 8937; 1399pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 429 BP; 99 A; 91 C; 104 G; 135 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB 2; Pred. No. 0.020; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 CACTCTTTTTTTTTTTTTTTTTTTTGG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 cactcttttttttttttttttttttgg 214
                                                                                                    Human polynucleotide SEQ ID NO 8937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.0%; S
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and podiagnosing and treating e.g. disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F
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2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-1989 (first entry)
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac
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                                                                                                                                                 cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C,
                                                                                                                                                 cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAO08946
                                                                                                                                                                                                                                                                                                                               WO200164835-A2.
                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2000;
18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation.
                                               06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001
AAI88877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ03970/c
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The invention relates to the human polypeptide-tyrosinase 14, the polynucleotide for coding it and the application of the polypeptide in tracting diseases including cancer, human immunodeficiency virus (HIV) infection.
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frote= "Site of insertion of the puromycin/bovine
frotth hormone poly-A signal sequence"
4852.4875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gal alpha(1,3) galactosyl transferase; gene targeting; transgenic animal; transplant rejection; immunomodulation; systemic lupus erythematosus; immune-heemolytic anaemia; collision intron targetting construct; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.0%; Score 29; DB 22; Length 1564; Best Local Similarity 100.0%; Pred. No. 0.017; Matches 29; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                    Polypeptide-tyrosinase 14 for treating e.g. cancer and human immunodeficiency virus (HIV) infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag- d
/note- "PCR primer as displayed in AAS02351"
complement (6911..6935)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "PCR primer as displayed in AAS02349"
complement (4827..4851)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= e
/note= "PCR primer as displayed in AAS02352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
/note= "PCR primer as displayed in AAS02350"
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1564 BP; 376 A; 377 C; 380 G; 431 T; 0 other;
                                                                                                                                                                                                                                                                                                         Claim 6; Page 23-24 (Disclosure); 31pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galactosyl transferase gene targetting vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443 CCACTCTTTTTTTTTTTTTTTTTTTTTT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      884 ccactctttttttttttttttttg 912
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235..260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS02362 standard; DNA; 11630 BP.
                                                                 99CN-0125656
                                                                                                 99CN-0125656.
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                                                                                                                                                                                                    WPI; 2001-530454/59.
P-PSDB; AAG78154.
                                                                                                                                   (UYFU-) UNIV FUDAN.
                                                                                                                                                                    Mao Y, Xie Y;
                                                                 21-DEC-1999;
                                                                                                   21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
CN1300743-A.
                                 27-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS02362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          New protein P25 prodn. - using P25 cDNA synthesised in vitro from ehrlich ascites tumour cell total mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complementary (c) DNA was transcribed from Ehrlich ascites tumour poly-A mRNA and subsequent hybridisation of this with oligonuclectide probes resulted in 2 clones. Of which I (P25b) comprised this sequence. The other clone (P25a) was altered at the translation start site by site-directed mutagenesis (at Nde I site). This was then used to transform host cells and the prod. is useful in eg medical research. See also AAQ03969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; polypeptide-tyrosinase 14; cancer; human immunodeficiency virus;
HIV; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 29; DB 11; Length 755; ilarity 100.0%; Pred. No. 0.019; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "polypeptide-tyrosinase 14"
/note= "claimed in claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 755 BP; 181 A; 228 C; 212 G; 133 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide-tyrosinase 14 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                           Gaestel M, Gross B, Benndorf R, Bielka H;
                                               Ehrlich ascites tumour; protein P25; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449 TTTTTTTTTTTTTTTTTTTTGGCTTCT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cocation/Qualifiers
                                                                                                                   Location/Qualifiers
                                                                                                                                                    /*tag= a
/label=P25 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI64562 standard; cDNA; 1564 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; fig 1; 6pp; German.
                                                                                                                                                                                                                                                                                                                                         (DEAK ) AKAD WISSENSCHAFT DDR.
                                                                                                                                                                                                                                                                      88DD-0168546.
                                                                                                                                                                                                                                                                                                       88DD-0316854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2001 (first entry)
                                                                                                                                   ..693
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-108215/15.
P-PSDB; AAR05780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                   Mus musculus
                                                                                                                                                                                                                                                                      17-JUN-1988;
                                                                                                                                                                                                                                                                                                       17-JUN-1988;
                                                                                                                                                                                                                                    01-NOV-1989
                 Clone P25b.
                                                                                                                                                                                                  DD273071-A.
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NAME OF THE PART O

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Gaps

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us-08-973-363-1.oli.rng

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Another The exon sequence is represented by dashes in the sequence presented in figure 1 in the specification and have been replaced with N's to maintain the sequence numbering"
                                                                                                                                                                                                                                                                                                                                                                                                   forther "The exon sequence is represented by dashes in the sequence presented in figure 1 in the septification and have been replaced with N's to maintain the sequence numbering"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In the sequence is represented by dashes in the sequence presented in figure 1 in the sequence presented in figure 1 in the specification and have been replaced with N's to maintain the sequence numbering"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number= 7
/note= "The exon sequence is represented by dashes
in the sequence presented in figure 1 in the
specification and have been replaced with N's to
maintain the sequence numbering"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //note="The exon sequence is represented by dashes
in the sequence presented in figure 1 in the
specification and have been replaced with N's to
maintain the sequence numbering"
                                                                                                                                                                                                              /number= 4
/note= "This sequence is specifically claimed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number= 8
/note= "This sequence is specifically claimed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "This sequence is specifically claimed in claim 16"
                                                                                                                                                                                                                                                                                                       complement (11688..11716)
 complement (3998..4020)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          maintain the 21766..27048
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/*tag= e
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13748..13810
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14359..14463
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                           /*tag= c
4852..4937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          claim 42"
                                                                                                                                                                                                                                                    claim 14"
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                                                                               /number=
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 primer_bind
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   The sequence represents Porcine Gal alpha(1,3) galactosyl transferase
gene targeting construct. The construct replaces exon 4
with the purconycin encoding gene. The invention relates to a method for
modulating the expression of a eukaryotic gene in a cell. The method
involves transfecting the cell with a nucleic acid construct. The
construct contains 2 nucleotide sequences which are portions of one or
more introns of the eukaryotic gene, and a sequence encoding a
selectable marker sequence is integrated into the gene
the expression of the marker results in modulation of
the expression of the construct is useful for making a
transgenic mammal. The construct is useful for reducing transplant
the transgenic mammal, and transplanting the harvested cells, tissue,
or organs into a patient in need. The knockout mammals produced by the
method are useful for screening drugs for immunomodulation (e.g for integral in the construct is useful for method are useful for screening drugs for immunomodulation (e.g for integral in the construct is useful for method are useful for screening drugs for immunomodulation (e.g for integral in the construct is useful for method are useful for screening drugs for immunomodulation (e.g for integral in the construct is useful for method are useful for method in the construct in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lupus erythematosus, rheumatoid arthritis and immune-haemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pig; Gal alpha(1,3) galactosyl transferase; intron 3-8; gene targeting; transpenic animal; transplant rejection; immunomodulation; systemic lupus erythematosus; immune-haemolytic anaemia; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                  Modulating the expression of a eukaryotic gene in a cell, involves transfecting the cell with a nucleic acid construct that disrupts at least a portion of the DNA sequence of the gene to be modulated -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 29; DB 22; Length 11630;
100.0%; Pred. No. 0.013;
ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11630 BP; 2956 A; 2688 C; 2693 G; 3290 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anaemia) and for producing proteins of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 10901 tctttttttttttttttttttggctt 10929
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1..4851
/*tag= a
                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 7; 86pp; English.
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                                                                         02-OCT-2000; 2000WO-US27065
                                                                                                               99US-0156953
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/number= 3
10..23
/*tag= b
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                                                                                                                                                      (ALEX-) ALEXION PHARM INC.
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                                                                                                                                                                                                                              WPI; 2001-266147/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 29; Conserv
WO200123541-A2
                                                                                                                 10-SEP-1999;
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                                     05-APR-2001
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                                                                                                                                                                                            Fodor WL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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intron
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98US-0104436.

15-OCT-1998;

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The sequence represents Porcine Gal alpha(1,3) galactosyl transferase introns 3.8, a gene used to make a gene targeting construct of the invention. The invention relates to a method for modulating the invention of a cutaryctic gene in a cell. The method involves transfecting the cell with a nucleic caid construct. The contains 2 nucleotide sequences which are portions of one or more introns of the eukaryctic gene, and a sequence encoding a selectable marker. The marker sequence is integrated into the gene sequence, so that expression of the marker results in modulation of the expression of the gene. The construct is useful for reducing transplant rejection by harvesting cells, tissue, or organs from the offspring of the transgenic mammal. The knockout mammals produced by the method are useful for screening drugs for immunomodulation (e.g for systemic lupus erthematosus, rhemmatoid arthritis and immune-haemolytic anaemia) and corpus proteins of interest.
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                                                                                                                                                          Modulating the expression of a eukaryotic gene in a cell, involves transfecting the cell with a nucleic acid construct that disrupts at least a portion of the DNA sequence of the gene to be modulated -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27048 BP; 6964 A; 5958 C; 6323 G; 7365 T; 438 other;
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                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 1; 86pp; English.
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Fodor WL, Ramsoondar JJ;
                                                                                  WPI; 2001-266147/27.
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AMA MANA126 to AMA45925 represent specifically claimed secreted expressed sequence tags (BESTS), isolated from human, mouse, chicken and rat tissues they were isolated from human, mouse, chicken and rat tissues they were isolated from The activities include: the Lissues they were isolated from. The activities include: chemotactic; proliferative; immunomodiatory; hamantopoiatel; chemotactic; proliferative; immunomodiatory; hamantopoiatel; chemotactic; analgesic; haemostatic; thrombolytic; antinifiammetory; chemokinetic; antibacterial; antifingal; antivital; antidiabetic; antisarthatic; unthearthisonian; antitiporiatic; cerebroprotective; cheropic; aftiparkinsonian; antitiporiatic; cerebroprotective; notropic; aftiparkinsonian; antitiporiatic; cerebroprotective; cherapy and in vaccines. The SESTs can be used for gene therapy and in vaccines. The SESTs can be used for gene defaultication and isolation of full-length change accoded by the SESTs can euseful in assays for determining biological activity and raising are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myelold or lymphoid cell deficiencies, wounds, burns, ulcers, catepoarthiitis, central nervous system disorders (casthma), thrombosis), inflammatory disorders (crohn's disease), tumours, bacterial, fungal or viral infections, depression and disease), tumours, bacterial, fungal or viral infections, depression and disease), tumours, bacterial, fungal or viral infections, depression and second disease).
                                                                                                                                                                                               Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (eSSTs), useful for treating various disorders such as autolimnue, infectious, and central nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó;
                                                                                      McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.9%; Score 28; DB 21; Length 450;
100.0%; Pred. No. 0.052;
Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                           Claim 1; Page 630; 803pp; English.
                                                                                                                 Bowman MR;
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                                            (GEMY ) GENETICS INST INC.
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nes 28; Conservative
                                                                                                              Treacy M,
                                                                                                                                                     WPI; 2000-317938/27.
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                                                                                                              Merberg D,
                                                                                      Jacobs K,
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2000US-0225268.
2000US-0225270.
2000US-0225447.
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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08-SEP-2000;
08-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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05-SEP-2000;
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08-SEP-2000;
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13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                          This sequence represents a prostate cancer specific nucleic acid sequence. The invention relates to a method for diagnosing cancer, tumour progression, hyperproliferative cell growth or accompanying biological and physical manifestations. The method involves contacting the biological sample with a probe that comprises a sequence capable of specification cany of the 339 nucleotide sequences given in the products and methods of the invention can be used for the diagnosis, prognosis, and treatment of cancer, tumour progression, hyperproliferations of the invention can be used for the diagnosis, properproliferative cell growth, and accompanying physical and biological manifestations. They can be used particularly for prostatic disorders such as metastatic prostate cancer, localised prostate cancer, or benign prostate hyperplasia (BPH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianemic; antiarthritic; cancer; antitheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
                                                                               Endege WO, Ford DM, Monahan JE, Schlegel R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                 New isolated prostate cancer specific nucleic acids, used to develop products for the diagnosis and treatment of cancer \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human nervous system related polynucleotide SEQ ID NO 10078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.9%; Score 28; DB 21; Length 499; 100.0%; Pred. No. 0.051; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 499 BP; 147 A; 115 C; 81 G; 154 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 CTTTTTTTTTTTTTTTTTTTTTTTTGGCTT 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 CTTTTTTTTTTTTTTTTTTTGGCTT 366
                                                                                                                                                                                                                Claim 12; Page 162; 212pp; English
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2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
98US-0088877
99US-0088877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                              Astel JH, Carroll E, F
Steinmann KE, Zhang J;
                                                (CHIR ) CHIRON CORP.
                                                                                                                                  WPI; 2000-116541/10.
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16-MAR-2000;
17-MAR-2000;
11-JUN-1998;
09-JUN-1999;
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24-FEB-2000;
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isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antigaonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rhematoid arthritis and ulcrative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.inf/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; antiinfly, antibacterial; vulnerary; antiparkinsonian; antisickling; antinanemic; antiarthritic; cancer; antiinflammatic; hepatotropic; cerebroprotective; antiinflammatory; antiilect; antiinflammatory; antiilect; antiinflammatory; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human nervous system related polynucleotide SEQ ID NO 13729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.9%; Score 28; DB 22; Length 626; Best Local Similarity 100.0%; Pred. No. 0.049; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 626 BP; 103 A; 181 C; 141 G; 201 T; 0 other;
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2000US-0186350
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2000US-0217487
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2000US-0224518
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02-MAR-2000; 2
16-MAR-2000; 2
17-MAR-2000; 2
19-MAY-2000; 2
19-MAY-2000; 2
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30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB1801) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are
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20-OCT-2000) 2000US-0240960.
20-OCT-2000) 2000US-0241786.
20-OCT-2000) 2000US-0241786.
20-OCT-2000) 2000US-0241786.
20-OCT-2000) 2000US-0241786.
20-OCT-2000) 2000US-0241786.
20-OCT-2000) 2000US-0241809.
20-OCT-2000) 2000US-024474.
08-NOY-2000) 2000US-0246474.
08-NOY-2000) 2000US-0246474.
08-NOY-2000) 2000US-0246476.
08-NOY-2000) 2000US-0246476.
08-NOY-2000) 2000US-0246523.
08-NOY-2000) 2000US-0246524.
08-NOY-2000) 2000US-0246524.
08-NOY-2000) 2000US-0246524.
08-NOY-2000) 2000US-0246524.
08-NOY-2000) 2000US-0246524.
17-NOY-2000) 2000US-0249211.
17-NOY-2000) 2000US-024921.
17-NOY-2000) 2000U
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14-Aug-2000; 2000us-0225214.

14-Aug-2000; 2000us-0225266.

14-Aug-2000; 2000us-0225267.

14-Aug-2000; 2000us-0225267.

14-Aug-2000; 2000us-0225270.

14-Aug-2000; 2000us-0225757.

14-Aug-2000; 2000us-0225757.

14-Aug-2000; 2000us-0225759.

18-Aug-2000; 2000us-0225759.

18-Aug-2000; 2000us-0225759.

22-Aug-2000; 2000us-0225759.

23-Aug-2000; 2000us-022588.

23-Aug-2000; 2000us-022984.

01-SEP-2000; 2000us-022984.

01-SEP-2000; 2000us-022943.

01-SEP-2000; 2000us-022944.

01-SEP-2000; 2000us-022944.

01-SEP-2000; 2000us-022914.

06-SEP-2000; 2000us-022914.

06-SEP-2000; 2000us-022914.

06-SEP-2000; 2000us-022914.

08-SEP-2000; 2000us-022914.

08-SEP-2000; 2000us-0231413.

08-SEP-2000; 2000us-0231414.

08-SEP-2000; 2000us-0231413.
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21-SEP-2000; 20000S-0234274.
25-SEP-2000; 20000S-0234997.
25-SEP-2000; 20000S-023484.
27-SEP-2000; 20000S-0235834.
27-SEP-2000; 20000S-0235834.
29-SEP-2000; 20000S-0235836.
29-SEP-2000; 20000S-0236367.
29-SEP-2000; 20000S-0236387.
29-SEP-2000; 20000S-0236387.
29-SEP-2000; 20000S-0236387.
29-SEP-2000; 20000S-0236387.
29-SEP-2000; 20000S-0236387.
20-CCT-2000; 20000S-0237038.
20-CCT-2000; 20000S-0237039.
20-CCT-2000; 20000S-0237039.
20-CCT-2000; 20000S-0237039.
20-CCT-2000; 20000S-0237039.
20-CCT-2000; 20000S-0234186.
20-CCT-2000; 20000S-0241869.
20-CCT-2000; 20000S-0241828.
20-CCT-2000; 20000S-0241828.
2000US-0224519
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14-SEP-2000; 2
14-SEP-2000; 2
14-SEP-2000; 2
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2000US-0249211. 2000US-0249212. 2000US-0249213. 2000US-0251988. 2000US-0256719. 2000US-02518479. 2000US-0251866. 2000US-0251869. 2000US-0251989. 2000US-0249215. 2000US-0249216. 2000US-0249217. 2000US-0249218 2000US-0249244 2000US-0246532 2000US-0246610 2000US-0246611 2000US-0246613 2000US-0249207 2000US-0249208 2000US-0249209 2000US-0249210 2000US-0249214 2000US-0249245 2000US-0249265 0000US-0249297 2000US-0249299 2000US-0249300 2000US-0250391 05-JAN-2001; 2001US-0259678 08-NOV-2000; 17-NOV-2000; 05-DEC-2000; 05-DEC-2000;

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 13729; 1701pp + Sequence Listing; English

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenita; (b) immune disorders e.g. Addison's disease, allergies, autoimmune harmolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and a parasitic infections.

Solution of the patent did not form part of the

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This sequence represents cDNA encoding the maize pathogen resistance-associated protein Mari. The maize Rarl protein has 794 homology to the barley Rarl protein over its entire length. The Rarl protein is required for the function of certain plant resistance (R) gene products which, along with pathogen avirulence (avr) gene products, mediate the hypersensitivity response (HR), a series of physical and physiological changes in host cells local to the site of infection which limits the spread of the infection. Rarl nucleic acids may be used in the generation of transgenic plants and seeds that exhibit increased expression of the Rarl protein. They may be used in this way to enhance resistance to a variety of pathogens, particularly viruses and fundi (e.g., powdery wheat, alfalfa, cotton, rice, barley, and millet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides, useful for improving the virus-resistance of plants such as maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, and millet, comprise nucleic acids encoding a Zea mays Rarl proteins
                                                                                                                                                                                                       Maize pathogen resistance-associated protein Rarl-encoding cDNA.
                                                                                                                                                                                                                                      Maize; Rarl; pathogen resistance-associated; plant; HR;
hypersensitivity response; viral infection; fungal infection;
transgenic; gene; ss.
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/product= "Maize Rarl protein"
713..929
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                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                 ABA02499 standard; cDNA; 1008 BP
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P-PSDB; AAM53060.
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5'UTR
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printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                 Gaps
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Local Similarity 100.0%; Pred. No. 0.048;
Les 28; Conservative 0; Mismatches 0; Indels
                                                                                                                     DB 22; Length 626; 0.049;
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                                                         Sequence 626 BP; 103 A; 181 C; 141 G; 201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human breast cancer expressed polynucleotide 3542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; breast cancer; cell marker; cytostatic; ss.
                                                                                                                     Match 3.9%; Score 28; DB Local Similarity 100.0%; Pred. No. 0.C es 28; Conservative 0; Mismatches
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ID AAL11085 standard; cDNA; 761
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24-MAR-2000; 2000US-0192099.
29-MAR-2000; 2000US-0193480.
15-MAY-2000; 2000US-0205320.
09-JUN-2000; 2000US-0211315.
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17-NOV-2000;
                                                                                                                                                                                                                                       Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25699
 951 TTTTTTTTTTTTTTTTTTTTTTTGGCTTC 924
                                                                                                     AAK70887 standard; DNA; 1086
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2000us-0226681.
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2000US-0229344
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2000US-0229513
2000US-0229513
2000US-0231243
2000US-0231243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with happropriate (I) expression. For example, they may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) supplement smy be used to product the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic-derived cells. AAK64703 csequences from the present invention. AMX64942 to AAK876950 and AAM82169 expressent thums immune/haematopoietic-antigen and AAM82169 crepresent sequences from the present invention.
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17-NOV-2000; 2000US-0249299.
17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0250160.
01-DEC-2000; 2000US-0250190.
05-DEC-2000; 2000US-0250198.
05-DEC-2000; 2000US-025198.
06-DEC-2000; 2000US-0251868.
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08-DEC-2000; 2000US-0251899.
11-DEC-2000; 2000US-0251990.
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and

for preventing,

metastasis

WPI; 2001-483426/52

Disclosure; SEQ ID NO 25700; 3071pp + Sequence Listing; English.

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2000us-0237038.
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2000US-0236370
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Ruben SM;

Barash SC,

Rosen CA,

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
concerns and extinity of (I) by expressing inactive proteins or to
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
colynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
concerns and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of heematopoietic-derived cells. AAK64703
concers and cancer metastases of heematopoietic antigen genomic
sequences from the present invention. AAK4942 to AAK54950 and AAM82169
represent sequences used in the exemplification of the present invention.
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20000S-0209467.
20000S-0214886.
20000S-0215135.
20000S-0215647.
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2000US-0180628.
2000US-0184664.
2000US-0186350.
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2000US-0190076
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02 - MAR - 2000;
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07-JUL-2000;
07-JUL-2000;
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28-JUN-2000;
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19-MAY-2000;
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000US-024182	0000S-024461	00000S-024647	00005-024647	0000S-024647	000US-024647	0000S-024652	20000S-0246524.	00003 024032	0000S-024652	000US-024652	000US-024653	000US-024660	00005-024661 00005-024661	000US-024661	000US-024920	000US-024920	0000S-024920	000US-024921	0000S-024921	00005-024921	0000S-024921	000US-024921	000US-024921	000US-024921	0000S-024921	00003-024324 000013-024924	000US-024926	000US-024926	000US-024929	0000S-024929	00005-025016	0000S-025039	0000US-025103	00003-025138	0000S-025147	000US-025185	0000S-025186	000US-025186	0000S-025198	0000S-025199	00005-025409	GENOME SCI INC.
0-OCT-20	1-NOV-200	8-NOV-200	8-NOV-200	8-NOV-200	8-NOV-200	8-NOV-200	08-NOV-2000;	8-NOV-200	8-NOV-200	8-NOV-200	8-NOV-200	8-NOV-200	8-NOV-200	8-NOV-200	7-NOV-200	7-NOV-200	7-NOV-2000	7-NOV-2000	7-NOV-2000	7-NOV-200	7-NOV-2000	7-NOV-2000	7-NOV-200	7-NOV-200	7 - NOV - 200 7 - NOV - 200	7-NOV-200	7-NOV-200	7-NOV-200	7 -NOV - 200	7-NOV-200 7-NOV-200	1-DEC-200	1-DEC-200	5-DEC-200 5-DEC-200	5-060-200	6-DEC-20	8-DEC-200	8-DEC-200	8-DEC-200	8-DEC-200	8-DEC-200	1 5	(HUMA-) HUMAN
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 38914; 3071pp + Sequence Listing; English.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM9191. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting

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the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK6763 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.9%; Score 28; DB 22; Length 1086; Best Local Similarity 100.0%; Pred. No. 0.045; Matches 28; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                Sequence 1086 BP; 312 A; 302 C; 233 G; 239 T; 0 other;
      SSSSSSX
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Search completed: August 3, 2002, 01:50:00 Job time: 32185 sec 5 ccactctttttttttttttttttttt 32 qq

443 CCACTCTTTTTTTTTTTTTTTTTT 470

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Gaps

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Run on:

Searched:

AZ589435 BG453842

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LOCUS
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MEDLINE
COMMENT
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A1630307
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
SOURCE
                                                                (without alignments)
1390.743 Million cell updates/sec
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A1916488 tz71d01.x
A2802813 2M0061B20
A1607901 ub60f03.x
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                                                                                                        1. CCCGGTCGGAGGTTTCAAGG......CTTGAAACCTCCCGACCGGG 723
                                                       August 2, 2002, 14:19:05; Search time 7016.61 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                 13736207 segs, 6748477542 residues
                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
                                                                                                                        OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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AL630307 382 bp mRNA linear EST 08-MAR-2000 ad080401.yl Proliferating Erythroid Cells (LCB:ad library) Homo sapiens cDNA clone ad08401 random, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Chemical Biology National Institute of Diabetes and Digestive and Kidney Diseases Building 10, Room 9B17, National Institutes of Health, Bethesda, MD 20892, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 382) and to 380, "N, Njoroge, "M,", Bouffard, G.G. and Miller, J.L. Gene expression in proliferating human erythroid cells Genomics 59 (2), 168-177 (1999)
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The 'ad' ilbrary was constructed by Alexander Gubin, Ph.D. in the The' ad' ilbrary was constructed by NIBMS, NIH. DNA Sequencing and/or analyses by National Biology, NIDMS, NIH. DNA Sequencing Center (NISC). More information available at:
Center (NISC). More information available at:
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Tel: 301 402 2373
Fax: 301 435 5148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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A2064574 RPCI-23-4 BI739401 603362030 AQ908063 GSSTC0873 AI744071 wc36a02.x BE652261 UT-M-AH0-BI404399 MI-P-CPI-

AZ064574 BI739401 AQ908063 AI744071

Result

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BH317627 CH230-159 BH314151 CH230-159 BH316471 CH230-159 AA946504 EST202003 BF472409 UT.M-BH3-AG144824 Pan trog1

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Mammalia; Eutheria;
1 (bases 1 to 313)
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Matches 30; Conservative
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AI916488
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Best Local Similarity
Matches 31; Conserv
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AZ802813/C
LOCUS
DEFINITION
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                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
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KEYWORDS
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                                                                                                                                                                                 cultured in the presence or absence of erythropoietin.
CD71+++ cells arising only in erythropoietin-supplemented
medium were isolated by fluorescence activated cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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/lab_host="DH5abha"
/note="Organ: blood; Vector: pCRII; Site_1: EcoRI; Site_2:
ECORI; Human peripheral blood mononuclear cells were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTC 04-FEB-2002
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                                                                                                                                                                                                                                                 sorting. Those cells demonstrated an average of six additional doublings in suspension culture and erythroid colony formation in methylcellulose. Suppression subtractive hybridization was used to construct the ad library (tester-sorted CD71+++ cells, driver-unsorted cells cultured without erythropoietin)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 37 Row: j Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4885172
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (0.7 FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.3%; Score 31; DB 9; Le
100.0%; Pred. No. 3.7e+02;
11ve 0; Mismatches 0;
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Homo sapiens, clone IMAGE:4762273, mRNA.
BC022284
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RESULT LOCUS

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COMMENT

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Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LML at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Lengh: 244 Fron: 0.00

Seq primer: -4019 from Gibco
High quality sequence stop: 222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon.9606"
/clone=lib="NaGE:294017"
/clone=lib="NaCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/tissue_type="adenocarcinoma"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                     AI916488 313 bp mRNA linear EST 16-DEC-1999 tz71d01.xl NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2294017 3',
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2M0061B20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0061B20 R, DNA sequence.
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Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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  Length 1130;
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7.5e+02;
4.3%; Score 31; DB 11; I ilarity 100.0%; Pred. No. 1.2e+02; Conservative 0; Mismatches 0;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
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361 bp DNA linear GSS 30-MAR-2000 RPCI-23-417J19.TJ RPCI-23 Mus musculus genomic clone RPCI-23-417J19 AZ064574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 361)
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 359) NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap. NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone was previously sequenced on the 5' end only, this new data is from the 3' end.
                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: ogapbs-remail.nh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_GSSs: RPCI-23-417J19.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="Inha@E1:8812"/
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/lab_host="nammary gland"
/lab_host="nammary gland"
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Unpublished (1999)
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100.0%; Pred. No. 6.5e+0
tive 0; Mismatches
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  IMAGE:1382141 3', mRNA sequence.
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Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/nesources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymeracecide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative aganose gel electrophoresis. Vector DNA was prepared from a derivative of pmost (gil4732114glbAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicilin resistance. "At a 72 c 77 g 93 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                               Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bubanalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 356)
Bunn, D., Aoyagi.A., Barber.M., Beacorn.T., Duval, B., Hamil.C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
hote="Vector: PWD4Day; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/clone="UUGC2M0061B20"
/clone="www.ee 10kb plasmid UUGCIM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.1%; Score 30; DB 12; Length 356; ilarity 100.0%; Pred. No. 6.6e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0061 row: B column: 20
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 TTTTTTTTTTTTTTTTTTTTTGGCTTCTT 478
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Location/Qualifiers
AZ802813
AZ802813.1 GI:12955136
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801 585 7177
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Gaps . 0

Length 359; 0; Indels

6.5e+02;

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/tissuc_type="retina"
/lab_host="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: Sali; cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NH_MGC Library."

3 59 C 85 9 98 t
/clone_lib="NIH_MGC_94"
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                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoR1: Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECOR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
74 c 63 g 158 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Email: szhaodetigr.org
Email: szhaodetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieterédejong.med buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Intercond (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11939 row: k column: 08
High quality Sequence stop: 364.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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4.1%; Score 30; DB 12; 1
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="65FBL/64"
/db_xref="taxon:10090"
/clone="RPCI-23-417J19"
/clone="RPCI-23"
/sex="Female"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5369215"
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                                                                                                                                                                                                                                           Class: BAC ends.
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BI739401
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JOURNAL
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Introduce Res. 10 (12), 1996-2005 (2000)

Typanosoma cruzi.

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.

I (bases 1 to 388)
Aguero.F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery

Accounted Res. 10 (12), 1996-2005 (2000)

Discharge 2056489
On Sep 14, 2000 this sequence version replaced gi:9370392.

Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                       GSSTC08733 Trypanosoma cruzi random genomic library Trypanosoma cruzi genomic clone G40N18, DNA sequence.
AQ908063
AQ908063
GSSTC08733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24 CP(1650) San Martin, Prov. de BS AS. Argentina Tel: 54-11-4580-7255 ext 309 Fax: 54-11-4752-9639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Trypanosoma cruzi"
/strain="CL-Brener"
/db.zref="taxon:5693"
/clone="G40N18"
/clone="Trypanosoma cruzi random genomic library"
/cell_type="epimastigote"
/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was randomly sheared using a nebulizer and the 1 to 2 Kb was gel purified and cloned into the dephosphoryated Hincil site of the vector"
                                                        Gaps
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  Length 364;
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4.1%; Score 30; DB 10; L
100.0%; Pred. No. 6.4e+02;
tive 0; Mismatches 0;
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6e+02;
                                                                                                         Email: dsanchez@iib.unsam.edu.ar
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us-08-973-363-1.oli.rst

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/organism="Mus musculus"
/drain=[G75BL/64]
/db_xef="taxon:10090"
/dlome="U1-w-AH0-act-g-04-0-UI"
/clone="U1-w-AH0-act-g-04-0-UI"
/clone="U1-w-AH0-act-g-04-0-UI"
/clone="U1-w-AH0-act-g-04-0-UI"
/clone="U1-w-AH0-act-g-04-0-UI"
/dev_stage="2-3" 2d days"
/dev_stage="vector: pT732D-pac (Pharmacia) with a modified
polylinker; ptem nouse cerebellum. The tag is a string of
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
/ 1996 Tissue provided by Ms. Annie Novakovich,
/ 21vic-Miller laboratories.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mEST@mail.nih.gov
CDNA Library Preparation: M. B. Soares Lab Clone distribution:
CDNA Library Preparation: M. B. Soares Ison RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP CDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements The following repetitive elements were
found in this CDNA sequence: 539-562, >POLY_A#Simple_repeat
                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
I (bases 1 to 516)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Sus scorfa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 535)
                                                                                                                                                                                                                                                                                                                                                             National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
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MI-P-CPL-nwz-b-06-0-UI.S1 MI-P-CP1 Sus scrofa cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.1%; Score 30; DB 10; Length 516; 100.0%; Pred. No. 4.5e+02; tive 0; Mismatches 0; Indels
UI-M-AH0-act-g-04-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
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                                               BE652261.1 GI:9978104
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Best Local Similarity
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TITLE
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BI404399
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Organ: Prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasanid DNA from the
normalized library NCI_CGAP_PT22 was prepared, and
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The diver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
Subtraction by Bento Soares and 1217928-1220615).
a 128 c 170 g 121 t
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                                                                                                                                                                                                               AI744071 S01 bp mRNA linear EST 17-DEC-1999 wc36a02.xl NCI_GGAP_Pr28 Homo septiens cDNA clone IAA6E:2317226 3' saintlar to contains element WSR1 repetitive element '; mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Primetes, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 501)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
     Gaps
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     0; Mismatches
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/organism="Homo sapiens"
/db_xref=taxon:9606"
/clone="IMAGE:2317226"
/clone_lib="NCI_CGAP_Pr28"
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                                                    449 TITITITITITITITITITITICGCTICTI 478
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                                                                                                                                                                                                                                                                                                                                    AI744071.1 GI:5112359
     30; Conservative
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Matches 30; Conserv
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BE652261/c
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EST 14-AUG-2001

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Gaps

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Best Local Similarity
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BH314151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="crossbreed"
/db_rref="taxon:9823"
/clone="MI-P-CPI-nwz-b-06-0-UI"
/clone_lib="MI-P-CPI-nwz-b-06-0-UI"
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/clone_lib="MI-P-CPI-nwz-b-06-0-UI"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT73D-Pac (Pharmacia) with a modified
/note="vector: pT73D-Pac (Pharmacia) with a MI-P-CP0
library is normalized library derived from the MI-P-CP0
library is normalized library derived from which this clone
was derived, please visit our web site at
/http://pleast.genome.lastate.edu/. The procedure used to
create this library has been previously described (Bonaldo
create this library has been previously described (Bonaldo
Lennon and Soares, Genome Research 6: 791-806, 1996)
                                                                                                                                                                                                                                                   The sequence contained an oligo-dr track that was present in the oligoucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Notl site and the oligo-dr track served to verify it as a clone from the normalized uterus library cDNA Library Preparation: M.B. Soares Lab , University of Iowa EST sequencing: M.B. Soares Lab , University of Iowa EST sequencing: M.B. Soares Lab , Lowa Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        БН417627 544 bp DNA linear GSS 03-DEC-2001 CH230-159G24.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-159G24, DNA sequence.
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Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: t \not\sim approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                       Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
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Pred. No. 4.3e+02;
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100.0%; Pred. No. 4...
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                                                                  Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sus scrofa"
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TAG_TISSUE=uterus
TAG_SEQ=AGTCCAATCG"
a 126 c 83 g
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1. .535
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Seg primer: M13 Forward
POLYA=Yes.
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Best Local Similarity 100.0
Matches 30; Conservative
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BH317627
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AUTHORS
TITLE
                                                               JOURNAL
MEDLINE
COMMENT
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Email: szhaoetigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/Dacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/Dacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/Dac_ends/rat/Dac_end_intro.html
Plate: 159 row: G column: 24
Seq primer: SP6
Class: BAC ends.
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Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn

A., Gebreqeorgis. E., Overton, L., Russell, D., Chen, D., Riggs, F., de

Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment

Uppublished (1999)

Other_GSSs: CH230-159A24.TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
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CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rat BAC End Sequences from Library CHORI-230 ECORI segment Unpublished (1999)
Other_GSSS: CH230-159G24.TV
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
7E1: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library
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Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0206
Fax: 301 838 0208
Email: szhao@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="BN/SsNHsd/MCW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. 544
/organism="Rattus norvegicus"
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Search completed: August 2, 2002, 22:41:29
Job time: 30144 sec
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Best Local Similarity 100.0
Matches 30; Conservative
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Rattus sp.
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1 (bases 1 to 573)
2 (bases 1 to 573)
2 (bases 1.2. Shetty, J., Shatsman, S., Tseqaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other_GSSs: CH230-159E22.TV
Context: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhaodeigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
avallability, please contact Pleter de Jong (pdejongémail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
BAT end primer: Sp6
Class: BAC ends.
availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPG Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 159 row: A column: 24 Seg primer: SP6 Class: BAC ends.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Rattus norvegicus"
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                                                                                                                                                 Location/Qualifiers
1. .560
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                                                                                                                                                                                                                                                                                                          /sex="Female'
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BH316471
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AA946504 585 bp mRNA linear EST 25-JAN-1999 EST202003 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone ROYAR90 3' end, mRNA sequence.
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/cell_Ltype="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHSd/McW) BAC library produced by
pieter de Jong"
a 194 c 129 g 147 t
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 585) Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D. Rat Genome Project: Generation of a Rat EST (REST) Catalog 6 Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="ROVAR90"
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//note="Organ: ovary; Vector: pT7T3Pac; Site_l: EcoRI; Site_l: Not!"
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Contact: Lee, NH
The Institute for Genomic Research
9712. Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-529
Fax: (301)-838-0208
Emai: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                    4.1%; Score 30; DB 12; Length 573;
100.0%; Pred. No. 4e+02;
ative 0; Mismatches 0; Indels
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OM of: US-08-973-363-6 to: GenEmbl:* out_format : pfs
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Query, US-08-973-363-6
Query length: 41
Database: GenEmbl:*
Database sequences: 1797656
Database length: 1873333701
Search time (sec): 4907.710000
                                                                           Date: Aug 3, 2002 4:25 AM
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score list:						FEATO
Sequence	Strd	Orig	ZScore	EScore	Len ! Documentation	
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gb_pat:A58696	+	187.00	487.82	8.3e-19		
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 6608)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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Other publication AU 5906996 961224.
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
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A58696
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A58691
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(bases I to 153)

(riffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS
BIRDS
PATENT: WO 9639505-A 2 12-DEC-1996;
PISIS INNOVATION (GB)
Other publication AU 5906996 961224.
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Gallus Gallus Gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianines; Gallus.

1 (Dases 1 to 6972)
Griffiths, R. and Korn, R.M.
A CHDI gene 1s Z chromosome linked in the chicken Gallus domesticus Gene 197 (1-2), 225-229 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF004397 6872 bp mRNA linear VRT 08-OCT-1997 Gallus chromo-helicase-DNA-binding on the 2 chromosome protein, variant with hydrophilic domain, (CHD-2) mRNA, complete
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Griffiths, R. and Korn, R.M.
Direct Submission
Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University,
Glasgow Gl2 800, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="chromo-helicase-DNA-binding on the 2 chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
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(Obsess 1 to 5947)
Woodge,T., Basral, M., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
Proc. Matl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="short insert found in longer variant mRNA of CHD-2" 1223~{
m c} 1520 g 1683 t
SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
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Percent Identity: 87.805
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/gene="CHD-2"
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Ratio: 4.561
Percent Similarity: 100.000
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US-08-973-363-6 x AF004397
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LOCUS AF006513
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4125 AAGCT.....CTTTCTGGTGCG 4141

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seq_name: gb_pr:AC092372
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2 (bases 1 to 5947)
Woodage,T.
Direct Submission
Submitted (03-JUN-1997) Laboratory of Gene Transfer, National Human
Genome Research Institute, National Institutes of Health, 49
Convent Drive, Bethesda, MD 20892-4442, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAB87381.1"
/db_xref="GI:2645429"
/translation="MNGHSDEESVRNSSGESSQSDDDSGSASGSGSSSSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQSGSSDSDSGSESGSQSESESDTSRENKVQARPPKVDGAEFWKSSPS1LAVQRSA1L
KKQQQQQQQQQQQQQSSSSSEDSSSSEDSSSSEVKRKKKKDEDWQMSGSGSPSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSDSESEEEREKSSCDETESDYEPKNKVKSRKPQNRSKSKNGKKILGQKKRQIDSSEE
DDDEEDYDNDKRSSRRQATVNVSYKEDEEMKTDSDDLLEVCGEDVPQPEEEEFETIER
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YHDHIKDRHQCDSYKRSDSRRRPYSSPGKOHDHDHHYKODSRYSSDREKHRKLIDDH
RSRDHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSESTHHKSSRDYRYHSDH
RASSSGPRSPLDQRSYGSRSPFEHSVPHKSTPBHTWSSRYT
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Percent Identity: 90.244
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/db_xref="taxon:9606"
/chromosome="5"
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/gene="CHD1"
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/gene="CHD1"
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Ratio: 4.579
nilarity: 92.683
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US-08-973-363-6 x AF006513
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AUTHORS
TITLE
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34 luAlaGlnArgLeuCysGlyAla 41

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Direct Submission

Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Dirive, Walnut Creek, C8 94598, USA

On Dec 7, 2001 this sequence version replaced gi:15290448.

Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-sigc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624.

The number of bases overlapped is 90404.
                       PRI 07-DEC-2001
                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101220)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
    AC092372 101220 bp DNA linear PRI 07-DEC
HOMO sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
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Percent Identity: 90.244
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/clone="RP11-58M12"
18862 c 17827 g 30409 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 101220)
DOE Joint Genome Institute.
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                                                                                         AC092372.3 GI:17402768
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US-08-973-363-6 x AC092372/rev
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Ratio: 4.579
Percent Similarity: 92.683
seq_documentation_block:
LOCUS AC092372
                                                                                                                                                              Homo sapiens
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75409 75508: gap of
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      AC012624 134365 bp DNA linear PRI 21-JUL-2001
Homo sapiens chromosome 5 clone CTD-2082117, complete sequence.
AC012624
                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 13456)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.
Location/Qualifiers
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhin1; Hominidae; Homo. 1 (bases 1 to 134365)
DOB JOAR Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 13435)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Percent Identity: 90.244
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/db_xref="taxon:9606"
/chromosome="5"
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AC021449.3 GI:10047806
HTG; HTGS_PHASE1; HTGS_DRAFT.
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DOE Joint Genome Institute.
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                                                                     AC012624.6 GI:14993679
                                                                                                                                                                                                                      Direct Submission
Unpublished
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4.579
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US-08-973-363-6 x AC012624
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seq_documentation_block:
Locus AC012624
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Percent Similarity:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                 Web site: http://www.jgi.doe.gov
                                                       Sequencing of Human Chromosome
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="CTC-480B11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="5
                                                                                                                                                                                                                                                                                    Project Information
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US-08-973-363-6 x AC008531
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Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE,
7 ordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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75509 92516: contig of 17008 bp in length 92517 92616: gap of 1000 bp 92617 106409: contig of 13793 bp in length 106410 106509: gap of 106510 143079: contig of 36570 bp in length. Location Qualifiers
                                                                                                                                                     /clone="RPI1-58M12"
/clone_lib="RPCI-11 Human Male BAC"
1. .38820
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 1
Percent Identity: 90.244
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26246 c 26678 g 45278 t
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                                                                                                                                                                                                                                                            38921. .40411
/note="assembly_fragment"
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/note="assembly_fragment"
47006. .51830
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/organism="Homo sapiens"
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HTG; HTGS_PHASE2; HTGS_DRAFT
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vector_side:left"
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4.579
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US-08-973-363-6 x AC021449
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Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q30
Consensus quality: 143744 bases at least Q30
Consensus quality: 143744 bases at least Q30
Consensus quality: 143744 bases at least Q30
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* This sequence will be replaced

* This sequence will be replaced

* This sequence will be preserved.

* The accession number will be preserved.

* 56175 56274: contig of 56174 bp in length

* 56175 100874: contig of 44600 bp in length

* 100875 100874: gap of unknown length

* 100875 113127: contig of 12133 bp in length

* 113128 113127: contig of 12133 bp in length

* 118291 118290: contig of 4963 bp in length

* 118291 118290: gap of unknown length

* 118795 123297: contig of 1304 bp in length

* 119795 123297: contig of 3503 bp in length

* 119795 123297: contig of 3503 bp in length

* 123298 123297: contig of 3503 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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Location/Qualifiers
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Percent Identity: 90.244
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Center clone name: CIT-HSPC_480B11
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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87658 ATTCTTCCAGATGATCCCGATAAAAACCACAAGCAAAAACAGTTGCAGAC 87707
                                                                                       1986 contigo of 148 bp in length 1966 app of unknown length 1968 2014: contig of 236 bp in length 2014: contig of 236 bp in length 2014: contig of 236 bp in length 2015; app of unknown length length 2015; app of unknown length 2015; app of unknown length 2016; app of unknown length 2017 contig of 458 bp in length 2017 contig of 5982 bp in length 2017; contig of 558 bp in length 2017; contig of 5514 bp in length 2017; contig of 5514 bp in length 2018; app of unknown length 2019; contig of 5514 bp in length 2019; contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib-"RPCI human BAC library 11"
35252 c 37061 g 60360 t 3202 others
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bp in length
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Percent Identity: 90.244
        contig of 1670 by
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of 2051
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/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-36012"
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouality: 174.00
Ratio: 4.579
nilarity: 92.683
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US-08-973-363-6 x AC091946
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110967
117572
117672
1123833
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130684
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131684
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12561
14612
14712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 157767 bases at least 040
Consensus quality: 180259 bases at least 030
Consensus quality: 180259 bases at least 030
Consensus quality: 184175 bases at least 030
Consensus quality: 184175 bases at least 030
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.79 in 020 bases; agarose-fp estimation
Quality coverage: 5.79 in 020 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence: It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                    AC091946 193446 bp DNA linear HTG 09-JUN-2001 Homo sapiens chromosome 5 clone RP11-36012, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (09-UNN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Ode: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19346)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5

Unpublished
                                           46770 ATTCTTCCAGATGCCCGATAAAAACCACAAGCAAAACAGTTGCAGAC 46819
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Center Project Name: 544799
Center clone name: RPCI-11_36012
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DOE Joint Genome Institute.
                                                                                                                                                                                             46870 AAGCT.....CTTTCTGGTGCG 46886
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AC091946.1 GI:14333882
HTG; HTGS_PHASE1.
                                                                                                                                              34 luAlaGlnArgLeuCysGlyAla 41
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Locus AC091946
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seq_documentation_block:
LOCUS AC022121 219258 bp DNA linear PRI 30-AUG-2001
BETNITION Homo sapiens chromosome 5 clone CTD-2007H13, complete sequence.
ACCESSION AC022121. 6 GI:15375145
                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 219258)
Direct Submission
Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 219258)
De Joint Genome Institute and Stanford Human Genome Center,
Direct Submission
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Submitted (30-4002-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
WWW. 191. doe. gov.
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 219258) DOE Joint Genome Institute and Stanford Human Genome Center.
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Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
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42062 c 40933 g 64309
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/db_xref="taxon:9606"
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      34 luAlaGlnArgLeuCysGlyAla 41
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SHGC-58345 G38487
SHGC-103595 G57841.
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                                                                                     seq_name: gb_pr:AC022121
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Homo sapiens chromosome 5 clone CTC-428111, complete sequence.
ACO26778
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DOE Joint Genome Institute.
DoE Joint Genome Institute.
Submitted (24 *MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jun 1, 2001 this sequence version replaced gi:13677045.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
STS Content:
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4.579 Gaps: 1
92.683 Percent Identity: 90.244
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/organism="Homo sapiens"
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SHGC-58345 G38487
SHGC-103595 G57841.
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LOCUS AC026778
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Consensus quality: 220677 bases at least Q40
Consensus quality: 255163 bases at least Q30
Consensus quality: 255163 bases at least Q30
Consensus quality: 255163 bases at least Q30
Consensus quality: 256799 bases at least Q20
Estimated insert size: 174820; agarose-fp estimation
Quality coverage: 8.62 in Q20 bases; agarose-fp estimation
Quality coverage: 5.55 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a Notking draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence ecord is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved
                                                                                                                                                                                                                                                      AC092382
Homo sapiens chromosome 5 clone RP11-75H1, WORKING DRAFT SEQUENCE, 47 unordered pieces.
AC092382
AC092382.1 GI:14589571
HTG; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

To (bases 1 to 276181)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5

Unpublished
contig of 1061 bp in length

gap of unknown length

contig of 1666 bp in length

gap of unknown length

contig of 1300 bp in length

contig of 1230 bp in length

contig of 1251 bp in length

contig of 1251 bp in length

contig of 1359 bp in length

gap of unknown length

gap of unknown length

gap of unknown length

gap of unknown length

contig of 137 bp in length

gap of unknown length

contig of 116 bp in length

contig of 116 bp in length

gap of unknown length

contig of 116 bp in length

gap of unknown length

gap of unknown length

contig of 115 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Joint Genome Institute
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Center clone name: RPCI-11_75H1
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DOE Joint Genome Institute
                                                                                                                               89350 AAGCT.....CTTTCTGGTGCG 89334
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PAT 06-MAR-1998
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS
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4.195 Gaps: 1
80.392 Percent Identity: 70.588
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224,
Location/Qualifiers
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/db_xref="taxon:32644"
40 c 31 q 24
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Sequence 3 from Patent W09639505.
A58684.1 GI:3714247
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"bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex determination; chromodomain-Helicase-DNA binding CHD-W; W chromosome; ss.
   /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/Na2001A.DAT:AAK73535
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAH41224
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:ABL34316
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:AAS69674
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:AAS993710
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Percent Identity: 80.392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse CHD-1 gene (bases 3855-977).
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ID AAT42756 standard; DNA; 153
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US-08-973-363-6 x AAT42756
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VARSBB + 167.00 46

VSSBB + 167.00 46

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AKBBB + 18.00 124

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SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal997.DAT:AAT47751 + 193.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal997.DAT:AAT47751 + 187.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal997.DAT:AAT47751 + 187.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal997.DAT:AAT47751 + 187.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal997.DAT:AAT47751 + 187.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal997.DAT:AAT47759 + 167.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal997.DAT:AAT47759 + 167.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal2001a.DAT:AAR88882 + 118.
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SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal2001a.DAT:AAR896071 + 60.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal2001a.DAT:AAR89003 - 58.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal2001a.DAT:AAR89003 - 58.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal2001a.DAT:AAR89003 - 58.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal2001a.DAT:AAR9003 - 58.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal2001a.DAT:AAR30569 - 58.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal2001a.DAT:AAR3059 - 58.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal2001a.DAT:AAR3059 - 58.
SIDSI/gcgdata/hold-geneseq/geneseqn-embl/Mal2001a.DAT:AAR3059 - 58.
SIDSI/gcgdata/hold-geneseq/genese
                                                                                                                                 version 4.5,
          out_format : pfs
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       N_Geneseq_032802:*
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Query length: 41
Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 523.620000
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Avian chromodomain-helicase-DNA binding genes determine sex
birds - used for sex determn. and to control sex of progeny
                                   1188 TCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG 1237
                  1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                  rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeuAlaLysArgG
                                                                                                                                                                                1238 AAGCACAGAGACTTGCTGGTGCA 1260
                                                                                                                                                 34 luAlaGlnArgLeuCysGlyAla 41
                                                                                                                                                                                                                                                 seq_documentation_block:
ID AAT42751 standard; cDNA; 6608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                 Chicken CHD-1A gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                  12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus sp
                                                                                                                                                                                                                                                                                                   AAT42751;
                                                                                                                                                                                                                                                                                                                                                                                                                 CHD-W;
                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                   The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a
                                                                                                                                                                                                                                                                                                                                                                                                                                Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                               seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                              40
                                                                                                               24 ysLeuLeuSerArgAspLeuAlaLysArgGluAlaGlnArgLeuCysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 41
Gaps: 0
Percent Identity: 87.805
                                                                                                                                                                                                                                                                                                                                                                                               Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                seq_documentation_block:
ID AAT42754 standard; cDNA; 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 187.00
Ratio: 4.561
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-DEC-1996
                                                                                                                                                                                                               151 GCG 153
                                                                                                                                                                                  41 Ala 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus sp.
                                                                                                                                                                                                                                                                                                                              AAT42754;
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sex determination; chromodomain-Helicase-DNA binding 1 Avian; chromodomain-Helicase-DNA binding on the W chromosome; ss.

BP.

(first entry)

Location/Qualifiers 228..5390

/*tag=

96WO-GB01341. 95GB-0011439

Tiwari B;

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The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT47751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo CDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A - Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or 2 chromosome. Probes based on CHD-W and CHD-1A give a W chromosome specific signal on hybridisation to genomic DNA of a non-rantite bird and can be used for sax determin. Of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 41
Gaps: 0
Percent Identity: 87.805
Claim 1; Fig 5; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 4.561
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 187.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
```

to: 1316

from: 1

Align seg 1/1 to: AAT42754

alignment_block: US-08-973-363-6 x AAT42754

Gaps: 1 Percent Identity: 70.588

4.19580.392

1 IleLeuProAspAspProAsp......

to: 153

from: 1

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Align seg 1/1 to: AAT42757
                                                                               alignment_block:
US-08-973-363-6 x AAT42757
   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT47757), chlcken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avian chromodomain-helicase-DNA binding genes determine sex in birds – used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bird; sex determination; chromodomain-Helicase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                 4130 CCGTGCAGACTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG 4179
                                                                                                     1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                           17 rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeuAlaLysArgG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
                                                    Align seg 1/1 to: AAT42751 from: 1 to: 6608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
52..81
                                                                                                                                                                                                                                                                                                                                                  34 luAlaGlnArgLeuCysGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID AAT42757 standard; DNA; 153 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-GB01341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95GB-0011439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS INNOVATION LTD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chick CHD-1A gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tiwari B;
US-08-973-363-6 x AAT42751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-043127/04.
P-PSDB; AAW08147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9639505-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT42757;
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determine
seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-14 (A - Avian) gene (AAT47275), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT47759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-18 gee also AAT42751) and CHD-W (see also AAT42751) and CHD-W (see also AAT42751) and cHD-W (see also AAT42754-55) genes determine
                                                                                                                                                                                                                                                        a
"bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŗ
                                                                                                                                                       Bird; sex determination; chromodomain-Helicase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                            Location/Qualifiers 52..81
                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Fig 3; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                 95GB-0011439.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS INNOVATION LTD.
                           seq_documentation_block:
ID AAT42758 standard; DNA; 153
                                                                                                                                                                                                                                                                                                                                                                                     96WO-GB01341
                                                                                                 (first entry)
                                                                                                                             Chick CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tiwari B;
                                                                                                                                                                                                                                                           /*tag=
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P-PSDB; AAW08148.
                                                                                                                                                                                                                            Key
misc_difference
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                                                                                               12-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1996;
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                                                                                                                                                                                                Gallus sp.
                                                                     AAT42758;
                                                                                                                                                         Bird;
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ī. V

51

Length:

alignment_scores: Quality: 172.00

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SXX CCCCCCXX S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                              Bird; sex determination; chromodomain-Helicase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                          50
                                                                                                                                                                1 ATTITACCIGATGATCCAGATAAGAAACCCCAGGCTAAGCAGTTACAGAC
                                                                                                                                                                                  8 .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL
                                                                        Gaps: 1
Percent Identity: 70.588
                          Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other;
                                                              Length:
                                                                                                                             to: 153
                                                                                                                                               1 IleLeuProAspAspProAsp......
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
52..81
                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                             Great tit CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID AAT42759 standard; DNA; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95GB-0011439
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                                                              172.00
4.195
80.392
                                                                                                                             Align seg 1/1 to: AAT42758
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/note= '
                                                                                                           US-08-973-363-6 x AAT42758
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                                                              Quality:
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misc_difference
                                                                       Ratio:
                                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1996;
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                                                     alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                           Parus major
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                                                                                                                                                                                                                                                                           151 GCA 153
                                                                                                  alignment_block:
                                                                                                                                                                                                                                                        41 Ala 41
                                                                                                                                                                                                                                                                                                                                          AAT42759;
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ds; human; telomere repeat binding factor; A-TRF; dimerisation domain; telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
                                          Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A - Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT4758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATTTTACCTGATGATCCAGATAAGAAACCACAGGCAAAGCAGTTGCAGAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 ysLeuLeuSerArgAspLeuAlaLysArgGluAlaGlnArgLeuCysGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL 24
                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 1
Percent Identity: 68.627
                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                    Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Altered telomere repeat binding factor 1 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 153
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1..1311
/*tag= a
/product= "A-TRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID AAV59280 standard; cDNA; 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US02765
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97US-0800264
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    IleLeuProAspAspProAsp.

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4.175
78.431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AAT42759
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US-08-973-363-6 x AAT42759
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                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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13-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-1998
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2000US-0209467.
2000US-0214886.
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2000US-0239935.
17 - MAR 2 2000)
18 - MAY - 2000)
19 - MAY - 2000)
30 - JUN 2 2000)
31 - JUN 2 2000)
32 - JUN 2 2000)
11 - JUL 2 2000)
14 - AUG 2 2000)
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29 - SEP - 2000)
20 - SEP - 2000)
    The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRP, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telahapeictasia. Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcertive colitis; infection; Hirschsprung's disease, chronic colitis; digestive system disorder; Meckel's diverticulum; ss.
                                                                                         Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/hold-geneseq/genesegn-embl/NA2001A.DAT:AAK88882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human digestive system antigen coding sequence SEQ ID NO: 1198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1237 ATTCTTCCAGATGATCCTGATAAAAACCACAAGCAAAAACGTAAGATTACAGAC 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 129.00 Length: 25
Ratio: 5.160 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAV59280 .from: 1 to: 1311
                                                                                                                                                                                   Claim 14; Page 110-111; 163pp; English.
Bianchi A, De Lange T, Van Steensel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAK88882 standard; cDNA; 421 BP.
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2000US-0184664.
2000US-0186350.
2000US-0189874.
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US-08-973-363-6 x AAV59280
                                  WPI; 1998-480769/41.
                                                       P-PSDB; AAW59280
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; colorectal cancer; colorectal cancer antigen; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AA157603
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 421 BP; 148 A; 78 C; 127 G; 61 T; 7 other;
                                                                                                                                                                                                                         Length: 35
Gaps: 0
Percent Identity: 68.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colorectal cancer antigen cDNA SEQ ID NO: 67.
                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 421
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ID AAI57603 standard; cDNA; 421
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2000US-0186350.
2000US-018974.
2000US-0198123.
2000US-0205515.
2000US-0205515.
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2000US-0217496.
2000US-0218290.
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2000US-0180628
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2000US-0216647
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2000US-0224519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                       118.00
4.069
82.857
                                                                                                                                                                                                                                                                                                                                                               to: AAK88882
                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-973-363-6 x AAK88882
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Ratio:
                                                                                                                                                                                                                                                              Percent Similarity:
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116-MAR-2000;
118-APR-2000;
119-MAY-2000;
07-JUN-2000;
07-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1198; 986pp; English
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P-PSDB; AAM93109.
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us-08-973-363-6.p2n.rng

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14-AUG-2000, 2000US-0225213.
14-AUG-2000, 2000US-0225214.
14-AUG-2000, 2000US-022526.
14-AUG-2000, 2000US-022526.
14-AUG-2000, 2000US-0225270.
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18-AUG-2000, 2000US-022977.
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18-AUG-2000, 2000US-02297.
17-SEP-2000, 2000US-02397.
18-AUG-2000, ```

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The present invention provides the protein and coding sequences of a mumber of colorectal cancer antigens. These are shown in AAL57547-AAL57619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen coding sequence of the invention.
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis ^{\circ}
 Claim 1; SEQ ID NO: 67; 522pp + Sequènce Listing; English.
 Rosen CA, Barash SC, Ruben SM;
 17.NOV-2000; 200005-0249299.
17.NOV-2000; 200005-0249299.
17.NOV-2000; 200005-0249300.
01.DEC-2000; 200005-0250391.
05.DEC-2000; 200005-0250391.
05.DEC-2000; 200005-0251988.
05.DEC-2000; 200005-0251988.
08.DEC-2000; 200005-0251895.
08.DEC-2000; 200005-0251896.
08.DEC-2000; 200005-0251896.
08.DEC-2000; 200005-0251896.
08.DEC-2000; 200005-0251899.
11.DEC-2000; 200005-0251899.
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200005-0249214.
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 2000US-0249244.
2000US-0249245.
2000US-0249264.
 (HUMA-) HUMAN GENOME SCI INC
 WPI; 2001-457727/49.
P-PSDB; AAM38625.
08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - NOV - 2000; 20 08 - DEC - 2000; 20 08 - D
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Seguence 421 BP; 148 A; 78 C; 127 G; 61 T; 7 other;

32

Length: Gaps:

alignment\_scores: Quality: 118.00 Ratio: 4.069

30

Length:

Quality:

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:ABL06443
 Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811.
 developmental biology; cell signalling; insecticide;
 Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
 Sequence 6240 BP; 1675 A; 1682 C; 1760 G; 1123 T; 0 other;
 1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
 17 rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeuAlaLysArgG
 Percent Identity: 68.571
 to: 421
 Myers EW;
 from: 1
 ВP
 PWD,
 ABL06443 standard; cDNA; 6240
 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
 23-MAR-2001; 2001WO-US09231
 (first entry)
 pharmaceutical; gene; ss.
 ŗ
 Align seg 1/1 to: AAI57603
 Drosophila melanogaster
 82.857
 alignment_block:
US-08-973-363-6 x AAI57603
 (ABB57737-ABB72072).
 Adams M,
 WPI; 2001-656860/75.
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 P-PSDB; ABB62340
Percent Similarity:
 WO200171042-A2.
 210 GGGCT 214
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 26-MAR-2002
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 Drosophila;
 27-SEP-2001
 Venter JC,
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alignment\_scores:

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is
 (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:ABL06442
 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
 Drosophila melanogaster expressed polynucleotide SEQ ID NO 13808
 Drosophila; developmental biology; cell signalling; insecticide;
 Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
 Sequence 9933 BP; 2711 A; 2468 C; 2538 G; 2216 T; 0 other;
 30
 Percent Identity: 56.667
 17 rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeu 30
 Length:
Gaps:
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 to: 6240
 Myers EW;
 from: 1
 BP.
 ABL06442 standard; cDNA; 9933
 PWD,
 23-MAR-2001; 2001WO-US09231.
 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
 (first entry)
 Ŀ
 pharmaceutical; gene; ss.
 Align seg 1/1 to: ABL06443
84.50
3.130
90.000
 Drosophila melanogaster.
 84.50
3.130
 US-08-973-363-6 x ABL06443
 Venter JC, Adams M,
 WPI; 2001-656860/75.
 seg_documentation_block:
 (PEKE) PE CORP NY
 P-PSDB; ABB62339
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Ratio:
 Ratio:
 Percent Similarity:
 WO200171042-A2.
 interactions
 alignment_scores:
 26-MAR-2002
 27-SEP-2001
 alignment_block:
 ABL06442;
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Ratio: 3.529

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The invention relates to polypeptides comprising an immunogenic part of a Leishmania and right associated DNA sequences, epitopes and fusion proteins are used in the production of compositions used for inducing a protective immune response against leishmaniasis, for prevention and treatment of the disease. The compositions can also be used generally to treat diseases that respond interleukin-15 stimulation. In addition, the products may contain an immunostimulant. The sequences represent companion and post primers used to amplify DNA of the invention.
 Leishmaniasis; Leishmania antigen; immunostimulant; protozoacide; Ldp23; luterleukin-15; PCR primer: Lbhsp83; M15; LF-1; LberF4A; Lmsp1a; Lmsp9a; MAPS-1A, LmgSP1; LmgSP3; LmgSP8; LmgSP8; LmgSP9; LngSP9; LngSP9; LcgSP9; Lcg
 New isolated Leishmania antigens, useful for prevention, treatment and diagnosis of leishmaniasis, also related nucleic acids for genetic
 Skeiky YAW, Bhatia A;
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:AAS96071
 6724 ATTTGCTTAACGAT...ACGCGCAAGCCCCAGGCCAAGCAGCAGCAGC 6770
 1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
 Sequence 1908 BP; 386 A; 531 C; 627 G; 358 T; 6 other;
Percent Identity: 56.667
 17 rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeu 30
 Campos-Neto A, Webb JR, Dillon DC,
 Align seg 1/1 to: ABL06442 from: 1 to: 9933
 Leishmania antigen 4G2-83 extended DNA.
 Claim 5; Page 190; 193pp; English.
 seq_documentation_block:
ID AAS96071 standard; cDNA; 1908 BP.
 05-APR-2001; 2001WO-US11254.
 05-MAY-2000; 2000US-0565501
14-AUG-2000; 2000US-0639206
 14-APR-2000; 2000US-0551974
 26-FEB-2002 (first entry)
Percent Similarity: 90.000
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 WPI; 2002-061971/08.
 (CORI-) CORIXA CORP
 Leishmania major.
 P-PSDB; AAU71861.
 WO200179276-A2.
 25-OCT-2001.
 vaccination
 Coler RM,
 AAS96071;
 Reed SG,
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Length:

60.00

Quality:

alignment\_scores

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The specification describes a method for the preparation of a collection of nucleic acids from organisms in a soil sample. The method comprises milling a dried sample to produce microparticles; suspending these in liquid buffer; extraction of nucleic acids from the microparticle; passing nucleic acid-containing solution through a microparticle; passing nucleic acid-containing solution through a microparticle; passing nucleic acid-enriched fractions through an anion exchange chromatography material; and recovering fractions containing purified nucleic acids. The nucleic acids are sources for sequences that encode either operons involved in a metabolic pathway (specifically polyketide synthesis) or polypeptides, particularly for production of therapeutic or agricultural compounds, especially polyketide antibiotics. ARP90034-39 represent open reading frames (ORFS) of the coding strand of cosmid
 Jeannin P, Pernodet J, Guerineau M, Simonet P, Courtois S;
Cappellano C, Francou F, Raynal A, Ball M, Sezonov G, Tuphile K;
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAF90036
 Collection of nucleic acids from environmental samples, useful for identifying e.g. genes encoding polyketide synthases and derived antibiotics
 Metabolic pathway operon, polyketide, polyketide antibiotic, type I polyketide synthase; ss.
 2 LeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnThrAr 18
 /product= "type I polyketide synthase"
 Nucleotide sequence of a type I polyketide synthase.
Gaps: 0
Percent Identity: 52.632
 Claim 35; Page 305-307; 356pp; French.
 Location/Qualifiers
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ID AAF90036 standard; DNA; 5292
 29-NOV-1999; 99FR-0015032.
07-JUN-2000; 2000US-0209800.
 27-NOV-2000; 2000WO-FR03311.
 06-AUG-2001 (first entry)
 ď
 (AVET) AVENTIS PHARMA SA.
 Align seg 1/1 to: AAS96071
 Percent Similarity: 89.474
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P-PSDB; AAB83973.
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 WO200140497-A2.
 Frostegard A;
 Unidentified.
 07-JUN-2001
 AAF90036;
```

present

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either operons involved in a metabolic pathway (specifically polyketide synthesis) or polypeptides, particularly for production of therapeutic or agricultural compounds, especially polyketide antibiotics. The present sequence represents cosmid a2691 coding strand), which encodes different
 The specification describes a method for the preparation of a collection of nucleic acids from organisms in a soil sample. The method comprises milling a dried sample to produce microparticles; suspending these in liquid buffer; extraction of nucleic acids from the microparticle;
 P, Courtois S;
Sezonov G, Tuphile K;
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAF90032
 Collection of nucleic acids from environmental samples, useful for identifying e.g. genes encoding polyketide synthases and derived antibiotics \, -
 Metabolic pathway operon; polyketide; polyketide antibiotic; ss.
 Sequence 34071 BP; 5791 A; 10858 C; 11089 G; 6333 T; 0 other;
 5 AspProAspLysLysProGlnAlaLysGln...LeuGlnThrArgAlaAs 20
 Nucleotide sequence of cosmid a26g1 (non-coding strand)
 to: 34071
 Length: 40
Gaps: 2
Percent Identity: 40.000
 Simonet E
Ball M, S
 from: 1
 Example 14; Page 274-288; 356pp; French.
 Guerineau M,
 Jeannin P, Pernodet J, Guerineau M,
Cappellano C, Francou F, Raynal A,
 to reverse of: AAF90033
 ВР
 17530 CCGCGGTTCGCCTGTGCGC 17511
 seq_documentation_block:
ID AAF90032 standard; DNA; 42717
 27-NOV-2000; 2000WO-FR03311.
 35 .. AlaGlnArgLeuCysGly 40
 29-NOV-1999; 99FR-0015032.
07-JUN-2000; 2000US-0209800.
 US-08-973-363-6 x AAF90033/rev
 (first entry)
 (AVET) AVENTIS PHARMA SA.
 2.231 65.000
 58.00
 polyketide synthases.
 WPI; 2001-374849/39.
 Quality:
 Percent Similarity:
 Ratio:
 WO200140497-A2.
 Frostegard A;
 06-AUG-2001
 alignment_scores
 07-JUN-2001
 alignment_block:
 Synthetic.
 Align seg 1/1
 AAF90032;
 88888888
 The specification describes a method for the preparation of a collection of nucleic acids from organisms in a soil sample. The method comprises milling a dried sample to produce microparticles; suspending these in liquid buffer; extraction of nucleic acids from the microparticle; passing nucleic acid-containing solution through a molecular sieve; passing nucleic acid-enriched fractions through an anion exchange chromatography material; and recovering fractions containing purified nucleic acids. The nucleic acids are sources for sequences that encode
 Simonet P, Courtois S; sall M, Sezonov G, Tuphile K;
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAF90033
 Collection of nucleic acids from environmental samples, useful for identifying e.g. genes encoding polyketide synthases and derived antibiotics -
 Metabolic pathway operon; polyketide; polyketide antibiotic; ss.
 34
 Sequence 5292 BP; 905 A; 1715 C; 1725 G; 947 T; 0 other;
 5 AspProAspLysLysProGlnAlaLysGln...LeuGlnThrArgAlaAs
 20 pTyrLeuIleLysLeuLeuSerArgAspLeuAlaLysArgGlu.....
 from: 1 to: 5292
 Nucleotide sequence of cosmid a26g1 (coding strand)
 Length: 40
Gaps: 2
Percent Identity: 40.000
encode type I polyketide synthases.
 Ball M,
 Example 14; Page 289-300; 356pp; French.
 Guerineau M,
 Jeannin P, Pernodet J, Guerineau M,
Cappellano C, Francou F, Raynal A,
Frostegard A;
 Align seg 1/1 to reverse of: AAF90036
 seq_documentation_block:
ID AAF90033 standard; DNA; 34071 BP.
 35 .. AlaGlnArgLeuCysGly 40
 07-JUN-2000; 2000US-0209800
 27-NOV-2000; 2000WO-FR03311
 99FR-0015032
 US-08-973-363-6 x AAF90036/rev
 06-AUG-2001 (first entry)
 (AVET) AVENTIS PHARMA SA
 2.231
65.000
 58.00
 WPI; 2001-374849/39.
 Percent Similarity:
 Quality:
 Ratio:
 WO200140497-A2.
 29-NOV-1999;
 alignment_scores:
 07-JUN-2001
 alignment_block:
a26g1, and
 Synthetic.
 AAF90033;
SXC
```

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passing nucleic acid-containing solution through a molecular sieve; passing nucleic acid-centiched fractions through an anion exchange chromatography material; and recovering fractions containing purified nucleic acids. The nucleic acids are sources for sequences that encode either operions involved in a metabolic pathway (specifically polyketide synthesis) or polypeptides, particularly for production of therapeutic or agricultural compounds, especially polyketide antibiotics. The present sequence represents cosmid along (non-coding strand). The sense strand encodes different polyketide synthases.
 Sequence 42717 BP; 8230 A; 13520 C; 13184 G; 7782 T; 1 other;
 5 AspProAspLysLysProGlnAlaLysGln...LeuGlnThrArgAlaAs 20
 alignment_scores:
Ouality: 58.00 Length: 40
Ratio: 2.231 Gaps: 2
Percent Similarity: 65.000 Percent Identity: 40.000
 Align seg 1/1 to: AAF90032 from: 1 to: 42717
 alignment_block:
US-08-973-363-6 x AAF90032
 8888888888888
```

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